

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:10:15 ; Search time 46 Seconds
(without alignments)
6365.237 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSPFKFVSTFAIFPLSM.....FELGSSRNYNVDLGAQYF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3991	83.6	772	16 Q9RB71	Q9rb71 chlamydia p
2	1923	40.3	926	16 Q823W9	Q823w9 chlamydophi
3	1915	40.1	926	2 P71135	P71135 chlamydophi
4	1805	37.8	942	16 Q823X1	Q823x1 chlamydophi
5	1748.5	36.6	866	16 Q823X0	Q823x0 chlamydophi
6	1667	34.9	841	16 Q822Q5	Q822q5 chlamydophi
7	1656.5	34.7	839	2 P77792	P77792 chlamydia p
8	1641.5	34.4	847	2 P71132	P71132 chlamydophi
9	1604.5	33.6	846	2 P71133	P71133 chlamydophi
10	1410.5	29.5	1011	16 Q823X5	Q823x5 chlamydophi
11	1237	25.9	602	2 Q8VU49	Q8vu49 chlamydia p
12	1219.5	25.5	601	2 Q8VL57	Q8vl57 chlamydia p
13	1186.5	24.9	843	16 Q823X3	Q823x3 chlamydophi
14	1175	24.6	700	2 Q8VU50	Q8vu50 chlamydia p
15	1172.5	24.6	581	2 Q8VU48	Q8vu48 chlamydia p
16	1161.5	24.3	843	16 Q823X2	Q823x2 chlamydophi

17	1116	23.4	868	16 Q823X4	Q823x4 chlamydophi
18	1103	23.1	591	16 Q7VQA1	Q7vqa1 chlamydia p
19	1020.5	21.4	445	16 Q7VQ99	Q7vq99 chlamydia p
20	1017.5	21.3	445	16 Q9RB67	Q9rb67 chlamydia p
21	935.5	19.6	649	2 P71134	P71134 chlamydophi
22	921	19.3	354	16 Q7VQA0	Q7vqa0 chlamydia p
23	916	19.2	359	16 Q9JSK6	Q9jsk6 chlamydia p
24	847	17.7	846	2 Q84FU0	Q84fu0 chlamydia t
25	843	17.7	846	2 Q84FU5	Q84fu5 chlamydia t
26	843	17.7	846	2 Q84FU2	Q84fu2 chlamydia t
27	841	17.6	846	2 Q84FU1	Q84fu1 chlamydia t
28	840	17.6	846	2 Q84FU4	Q84fu4 chlamydia t
29	838	17.6	846	2 Q84FU3	Q84fu3 chlamydia t
30	835	17.5	846	2 Q83TT8	Q83tt8 chlamydia t
31	834	17.5	846	2 Q83U50	Q83u50 chlamydia t
32	833	17.4	846	2 Q84FT9	Q84ft9 chlamydia t
33	832	17.4	846	2 Q84FT8	Q84ft8 chlamydia t
34	831	17.4	846	2 Q84FT7	Q84ft7 chlamydia t
35	821	17.2	494	16 Q9RB68	Q9rb68 chlamydia p
36	792	16.6	427	16 Q9RB70	Q9rb70 chlamydia p
37	768	16.1	177	16 Q7VQA2	Q7vqa2 chlamydia p
38	768	16.1	186	16 Q9RB72	Q9rb72 chlamydia p
39	717	15.0	934	16 Q824E6	Q824e6 chlamydophi
40	676.5	14.2	1537	16 Q821X9	Q821x9 chlamydophi
41	673	14.1	941	16 Q823Y1	Q823y1 chlamydophi
42	658.5	13.8	981	16 Q823X6	Q823x6 chlamydophi
43	655	13.7	1795	16 Q824E7	Q824e7 chlamydophi
44	644.5	13.5	936	16 Q823Y2	Q823y2 chlamydophi
45	614.5	12.9	980	2 Q84FU6	Q84fu6 chlamydia t

ALIGNMENTS

RESULT 1

Q9RB71 PRELIMINARY; PRT; 772 AA.
 ID Q9RB71
 AC Q9RB71;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pmp 3 [Outer membrane protein 5].
 GN PMP 3 2 OR CPB0018.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria: Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA."
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TW-183;
 RA Geng M.M., Schuhmacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 other Chlamydia strains based on whole genome sequence analysis."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AF002545; BAA98226.1; -;
 DR EMBL; AF017157; AAP97951.1; -;
 DR PIR; H86492; H86492.
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF02415; Autotransporter; 1.
 DR Pfam; PF02415; Chlamydia_PMP; 1.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP_repeat; 6.

SQ	SEQUENCE	772 AA; 82931 MW; 484FC56D635801EBB CRC64;
Query Match	83.6%; Score 3991; DB 16; Length 772;	
Best Local Similarity	99.9%; Pred. No. 6.8e-175;	
Matches 771; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	
QY	157 LFFKNTSTNGGALTAKTLSTLTGTTMSALFSENTSSKKGGAIQTSALITITGNQGEVSF 216	
DB	1 MLFKNSTNGGALTAKTLSTLTGTTMSALFSENTSSKKGGAIQTSALITITGNQGEVSF 60	
QY	217 SDNTSSDGAAPTEASVTISNNAKVSPIDNKVTGASSSTTGDMSGGAIQTSALITITGNQGEVSF 276	
DB	61 SDNTSSDGAAPTEASVTISNNAKVSPIDNKVTGASSSTTGDMSGGAIQTSALITITGNQGEVSF 120	
QY	277 TLGNQMLLFNNSTSTAGGAIYVKLELASGLTLFRNSVNGTAPKGAIAIEDSGE 336	
DB	121 TLGNQMLLFNNSTSTAGGAIYVKLELASGLTLFRNSVNGTAPKGAIAIEDSGE 180	
QY	337 LSLGADSGDIVFLGNVTSTTPGNNRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGST 396	
DB	181 LSLGADSGDIVFLGNVTSTTPGNNRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGST 240	
QY	397 TVTDVLKNETPADSALQYTGNIIPTEGKLSSETAADSKNLTSKLLQVTLSCGTLISLKH 456	
DB	241 TVTDVLKNETPADSALQYTGNIIPTEGKLSSETAADSKNLTSKLLQVTLSCGTLISLKH 300	
QY	457 GVTIQTQAFQOADSRLMDVGTTLLEPADTSTINNLVINISIDCAKAKIETKATSKNL 516	
DB	301 GVTIQTQAFQOADSRLMDVGTTLLEPADTSTINNLVINISIDCAKAKIETKATSKNL 360	
QY	517 TILSGTITLLDPTGTFYENHSLRNQSYDILELKASGTVTSTAVTTPDPIMGEKHFYGYQT 576	
DB	361 TILSGTITLLDPTGTFYENHSLRNQSYDILELKASGTVTSTAVTTPDPIMGEKHFYGYQT 420	
QY	577 WGPVWGTGASTATFNWTKGYIIPNPERIGSLVNSLWNAFIDISSLHYLMETANEGLQ 636	
DB	421 WGPVWGTGASTATFNWTKGYIIPNPERIGSLVNSLWNAFIDISSLHYLMETANEGLQ 480	
QY	637 GDRFWCAGLSNFFHKDSTKRRGRHLGGVVGIGNLHTCSDKILSAAPCOLFCRDY 696	
DB	481 GDRFWCAGLSNFFHKDSTKRRGRHLGGVVGIGNLHTCSDKILSAAPCOLFCRDY 540	
QY	697 FVAKNQGVYGGTLYQHNETYISLPCKRLPCSLSYVPTPEIPLVPSGNLSYTHTDNLKT 756	
DB	541 FVAKNQGVYGGTLYQHNETYISLPCKRLPCSLSYVPTPEIPLVPSGNLSYTHTDNLKT 600	
QY	757 KYTTPTVKSGWNSFALFEGGRAPICLDESALPEQYMPFMKLOFYVAHQGFKEQTE 816	
DB	601 KYTTPTVKSGWNSFALFEGGRAPICLDESALPEQYMPFMKLOFYVAHQGFKEQTE 660	
QY	817 AREFGSSRLVNLALPIGIRFDKESDCODATYMLTGYTVDLVRSNPDCTTTLRISGDSWK 876	
DB	661 AREFGSSRLVNLALPIGIRFDKESDCODATYMLTGYTVDLVRSNPDCTTTLRISGDSWK 720	
QY	877 TFGTNLARQALVLRAGNHCFNSNFEAFQSFELRGSSRNYNVDLGAQYQF 928	
DB	721 TFGTNLARQALVLRAGNHCFNSNFEAFQSFELRGSSRNYNVDLGAQYQF 772	
RESULT 2		
Q823W9	PRELIMINARY; PRT; 926 AA.	
ID	Q823W9	
AC	Q823W9;	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Polymorphic outer membrane protein G family	
DE	protein/autotransporter.	
GN	CCA00284.	
OS	Chlamydia caviae.	
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.	
OX	NCBI_TaxID=83557;	
RN	[1]	

RP	SEQUENCE FROM N.A.	
RC	STRAIN=GPIC;	
RX	MEDLINE=22569155; PubMed=12682364;	
RA	Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,	
RA	Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carly H.A.,	
RA	Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,	
RA	Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoli P.M.,	
RA	Fraser C.M.;	
RT	"Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):	
RT	examining the role of niche-specific genes in the evolution of the	
RT	Chlamydiaceae.";	
RL	Nucleic Acids Res. 31:2134-2147 (2003).	
DR	EMBL; AB016995; AAP05035.1; -.	
DR	TIGR; CCA00284; -.	
DR	InterPro; IPR006315; Autotransport.	
DR	InterPro; IPR005546; Autotransporter.	
DR	InterPro; IPR003368; Chlamydia PMP.	
DR	Pfam; PF03797; Autotransporter; 1.	
DR	Pfam; PF04415; Chlamydia_PMP; 1.	
DR	TIGRFAMs; TIGR01414; autotrans_bar1; 1.	
DR	TIGRFAMs; TIGR01376; POMP_repeat; 5.	
KW	Complete proteome.	
SQ	SEQUENCE 926 AA; 98213 MW; 0E1062E0778658B2 CRC64;	
Query Match	40.3%; Score 1923; DB 16; Length 926;	
Best Local Similarity	43.2%; Pred. No. 3.8e-80;	
Matches 412; Conservative	149; Mismatches 339; Indels 54; Gaps 17;	
QY	1 MKSSPPKVFESTFAIFPLSM-----TATETVLDSASFQGNKGNFSVRESQEDA 50	
DB	1 MRPSLYKILISTLTIPLSFHSQVHAEVALTQESVLD-----NGAFSPQSTAG 52	
QY	51 GTTYLFKGNVTLENIIPGTGTAITKSCFNNTKGLDFTTGNNSLLFTQVDAGTVAGAAVNS 110	
DB	53 GTTYNVESDISIVD-ACQAAAAMVSAAFVQTADDLTFKNGRSLALENVSGANPG-AIYV 110	
QY	111 SVVDSKSTTFIGSSLSPIASPCSSITTCGKAVSCSTGSLTKVNSLLFSKNFSDNGGA 170	
DB	111 SAADKTLTLTDFSTLSFKKCPKHTVNTGKAVK-SGGALNLANNAASILFNQHSADGGA 169	
QY	171 ITAKTSLTGTMTSALFSENTSSKKGAIQTSALITITGNQGEVSFSDNTSSDGAAPFT 230	
DB	170 ISCKAFSLTGSKSEISFTNTSTKGGALAAATGVANLSDNQKVFSGNTAVNSGGAVYA 229	
QY	231 EASVTISNNAKVSPIDNKVTGASSSTTGDMSGGAIQTSALITITGNQGEVSFSDNT 290	
DB	230 EANTTIAGNSAVVFNNAVTG-----TIDCGCGAIHCSKTGATPVLITRDNKVLFPKNT 284	
QY	291 STTAGGAIYVKLELASGLTLFRNSVNGTAPKGAIAIEDSGELSLSDSGDIVFLG 350	
DB	285 SAAKGGAIYADKLYLTSGGPTVFGNKAT-NAAPKGAIGIAANGECSTAEHGDITFEN 343	
QY	351 NVTVTSTPGT-NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGSTTVDLVKNETPA 409	
DB	344 NLIATANNATVKNAINIBGNKGFYNLRAASGNTLTFYDPIVVG--TAADLLTLNQ--A 399	
QY	410 DSALQYTGNIIFTGKLSSETAADSKNLTSKLLQVTLSCGTLISLKHGTLQTAQTOA 469	
DB	400 EGTQVYNGRIIFSGEKLTDQADADNLKTVFTQPIALAAAGELIENGVEVEKAVSQTA 459	
QY	470 DSRLEMDVGTTLLE-PADTSTINNLVINISIDGAKKAKIETKATSKNLTSGLTITLLDPT 528	
DB	460 GSLILIDAGTKLSAKTEDVTLTNLAIPNSLDGTKIATVAANNAKNTVTGAIGIIDPT 519	
QY	529 GTFFYENHSLRNQPSYDILELKASGTVTSTAVTTPDPIMGEKHFYGYQGTWGPVW----GT 584	
DB	520 GKFYEDKLNELTALGGIOFSKAGSITTTDVPSTTTRSPAQHYGYQGNNS-LSWITDNGS 578	
QY	585 GAST-TATFNWTKGYIIPNPERIGSLVNSLWNAFIDISSLHYLME-TANEGLQGAPAFW 642	
DB	579 DPKTQTAVFNWNTKGYNPNPERRAPILVNLNSLWGSFMDIRSIQDVMSERSVDTLLETARKGL 638	
QY	643 CAGLSNFFHKDSTKRRGRHLGGVVGIGNLHTCSDKILSAAPCOLFCGRDRDYFVAKNQ 702	

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Db 639 VSGVGNELHDKPSAENRKKFRHISGVLGATNTTSQEDTILSVAFQKDKOVLVAKNA 698
QY 703 GTVYGGTLYXQHNETYISL-----PCKLRPCSLSYVTEIPVLFSGNLSYTHNDL 754
Db 699 ANVAGSIYYQHVKFDDLTFLNGPNTC-----CSGFSKEIDIFILDAQVTYCHTNNM 752
QY 755 KTKYTYTFTVKGSGWGNDSFALEFGGRAPICLDESALFEQYMPFMKLOFVVAHQGFKEQG 814
Db 753 TTTYTDPEVKGSGWNTVGVALSTSVPIPIFTHAFDVSAPPFAKLQVVAHQDFKEPT 812
QY 815 TEAREFGSSRLVNLALPIGIRFDKESQDQATYMLTGYTVDLVRSNPDCTTLIRISGDS 874
Db 813 REGRTFESSDLLNVSPVIGVKFKLVGKTAAYDLTLMYVDPVYRHNPCITGFAINDVT 872
QY 875 WKTFGTNLARQALVLRAGNHCFCNSFEAFSOFSEFELRGSSRNYNVDLGAKYQF 928
Db 873 WLTIATNLARQAFIIRAGNHIATVSGFEMFSQGFELRSSRNYNVDLGAKVSP 926

RESULT 3
P71135 PRELIMINARY; PRT; 926 AA.
AC P71135;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative 98 kDa outer membrane protein.
OS Chlamydia abortus.
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83555;
RN [1]
RP STRAIN=ovine abortion S26/3;
RC Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT '98kDa protein genes from ovine abortion strain S26/3 Chlamydia
RT psitacal.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72499; AAB18188.1; -.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF023797; Autotransporter; 1.
DR Pfam; PF02415; Chlamydia_PMP; 2.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 6.
SQ SEQUENCE 926 AA; 98439 MW; 3E755E2F594750F CRC64;

Query Match 40.1%; Score 1915; DB 2; Length 926;
Best Local Similarity 42.9%; Pred. No. 8.8e-80;
Matches 410; Conservative 156; Mismatches 333; Indels 56; Gaps 18;

QY 1 MKSFFPKFVSIFAIFLSM-----IATETVLDSSASFDGKNGKNGFVSRESQEDA 50
Db 1 MPRLYKILISLTLLIPIGFHFSQLHAVALTQESILDA-----NGAFSPQSTAG 52

QY 51 GTTYLFGKVNLENIPGTGTAIKCFNNTKGDLTFTGNSNLLFQTVADAGTVAGAAVNS 110
Db 53 GTIYNVESIDIVDVGQAALASSAFVQADNLTFKGNHLSLITNANAG-ANPAGINV 110

QY 111 SVVDKSTTFIGFSSLSFIASPGSSITGKAVSCSTGSLTKNVLSLFSKPFSTDNGGA 170
Db 111 NTADKILITLDFSKLSEKPCPSLVNTGKAMK-SGGALNLANNASILPDQNYSAENGGA 169

QY 171 ITAKTILSLGTWMSALFSENTSSKGAICTSDALLITGNQGEVSFSDNTSSDGAIFT 230
Db 170 ISCKAFSLTGSSEKISFTTNTAKKGAAATGIAHLSDNQGTIFRSGNTAVNSGAVYS 229

QY 231 EASVTISNNAKVSFIDNKVTGASSITGDMGSGAICAYKTTSTDKVTLTGNOMLFSSNT 290
Db 230 EASMTIAGNNHVAFNSNVAVGSS-----DCCGAIHCSTKGTGAPTITRDKNVLFEEWT 284

QY 291 STTAGGAIYVKLELASGGLTLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLG 350
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Db 285 SSAAGGAIYTDKILTLTSGGPTAFNNKVTHAT-PKGAIGAANGECSLTRAHEGDIITFDN 343
QY 351 NTVTSTTPGT-NRSSIDLGTSAKMTALRSAGRAIFYDPIITTSSTTVTDVLKVNETPA 409
Db 344 NLMATQDNATIKENAINIEGNGKFNVLRAASGKTI SFYDPIITVEGN--AADLLTLNKAEG 401
QY 410 DSALQYTGNIITFCEKLSSETAADSKNLTSLKLPVTLISGGLSLKGVTLQOAFQQA 469
Db 402 DKT--YNGRIIFSGEKLTVEQAAVADNLKTTFTQPIITLAAGELVIRSGVEFAKTVVQTA 459
QY 470 DSRLEMDVGTLE--PADTSTINNVLINISSIDGAKAKIETKATSKNLTLSGTTILDDPT 528
Db 460 GSLILMDAGTKLSAKTUEDATLNLAINPNTLDGKPAVDVAAGKNVTLISGALGVIDPT 519
QY 529 GTYENHSLRNPOSYDILELKASGTVTSTAVTDPDIMG-BKPHYGYGTWGPVW----- 582
Db 520 GKFEYENHKLNDTLALGGIQLSGKGSVTTINV-PSHVVGVVAETHYGYQGNWS-VSWVKDNN 577
QY 583 GTCASTATATNTKTYIPIPNRIGSLVPSNLWNAFIDISSLHYLMETANEG-LOGDRAF 641
Db 578 SDPKTOTALTFTWNTKTYVPNPERRAPLVLSLWMSFIDLSIQDVLERSVDSILETRGL 637
QY 642 WCAGLSNFFHKDSTKTRRGFRHLSGGYVIGGNLHTCSDKILSAAFCOLFCORDRDYFVAKN 701
Db 638 WVSGIGNFFHKORNAENRKRHISGVLGATNTSEDSLSVAFQKFAKDKDYLVSKN 697
QY 702 QGTVYGGTLYXQHNETYISL-----PCKLRPCSLSYVTEIPVLFSGNLSYTHND 753
Db 698 AANVYAGSVYVQHVSKFPDDLTRLFNGPNTC-----CSGFSKEIPILDAQITVCHTANN 751
QY 754 LKTKYTYTFTVKGSGWGNDSFALEFGGRAPICLDESALFEQYMPFMKLOFVVAHQGFKEQ 813
Db 752 MTSYTDPEVKGSGWNTLGLTSTVPIPVFSSIFDSYAFPAKLQVVAHQDDPFKEP 811
QY 814 GTEAREFGSSRLVNLALPIGIRFDKESQDQATYMLTGYTVDLVRSNPDCTTLIRISG 873
Db 812 TTEGRVFESSDLLNVSPVIGIKELSYGERSAYDLTLMYIPDYRHNPCMTGLAINDV 871
QY 874 SWKTFGTNLARQALVLRAGNHCFCNSFNFAFOSFELRGSSRNYNVDLGAKYQF 928
Db 872 SWLTATNLARQAFIVRAGNHIALTSGVEMFSQGFELRSSRNYNVDLGAKVAF 926

RESULT 4
Q823X1 PRELIMINARY; PRT; 942 AA.
AC Q823X1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polymorphic outer membrane protein G family protein/autotransporter, putative.
DE CCA00282.
OS Chlamydia caviae.
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RC MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., Heideberg J., Holtzapple E., Khouri H., Federova M.B., Carty H.A., Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavol P.M., Fraser C.M.;
RA "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiales.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; A601695; AAP05033.1; -.
DR TIGR; CCA00282; -.
DR InterPro; IPR003368; Chlamydia_PMP.
```


OS Chlamydia psittaci (Chlamydophila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OVINE ENZOOTIC ABORTION ISOLATE S26/3;
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U65943; AAC15924.1; -;
DR EMBL; U65942; AAC15922.1; -;
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMs; TIGR01414; autotrans_barl; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW SIGNAL.
FT CHAIN
SQ SEQUENCE 839 AA; 89824 MW; 4581C7CBAF7FF4C4 CRC64;

Query Match 34.7%; Score 1656.5; DB 2; Length 839;
Best Local Similarity 40.3%; Pred. No. 5.3e-68;
Matches 381; Conservative 133; Mismatches 285; Indels 147; Gaps 24;

QY 11 STEAIPPLSMI-ATETVLDSASFGN-KNGNFSVRESQEDAGTYLFGKGVNLTENIGT 68
DB 13 SLFASNSLFANDACTALTPDSYNGNVTSEFQVKEI--SSGTYTCEGNVCI-SFAGK 69

QY 69 GTAIKSCFNNTKGLTFTGNSLLFQTVDAAGTAVAGAAVNSVVDKSTFTFGSSLGFI 128
DB 70 DGLKKSCFSAT-DNLTFLNGYLLCFDNIITTSANPGAINVOGKTLGSGFSLFSCA 128

QY 129 ASPGSIITKGAVSCSGSLTKNLSLFKNSFTDNGGAIKTLSLTGTTMSALFS 188
DB 129 YCPPG--ITGYGAIQ-TKGNITLKDNSSLVFHKNCSTAEAGGAIQC----- 170

QY 189 ENTSSKKGAIQTSALLITNGQGEVFSFSDNTSSDGAIAIFTEASVTISNNAKVSEIDNK 248
DB 171 ----- 170

QY 249 VTGASSTTGDMGGCAICAYKTSTDTKVTLTGNQMLFSNNTSTTAGGAIYVKLELASG 308
DB 171 -----KGSSDAELKIENQNLVFSNSSTSKGGAIVADKLTIVSG 210

QY 309 GLTLFSRNSVNGGTAPKGAIAIED-SGELSLSADSGDIVFLGNTVTSTTPGNT---RSS 364
DB 211 GPTLFSNNSVNGSSPKGGAISIKDSGECSLTADGLDITFDGKIIKTSGGSSVTWRNS 270

QY 365 IDLGSATKMTALRSAGRAIIFYDITGSSSTVTDVLKVNTPADSALOHTGNLIIFGCE 424
DB 271 IDLGT-GRFTKLRAKDGFIFDITGGS-----DELNINK---KETVDYTGKIVFSGE 322

QY 425 KLSSEADSKNLSKLLQPVTLTSGTSLKHGVTLQTOAFTQQAQDSRLMDVGTTLBP- 483
DB 323 KLSDEKARAENLSTFNPITLSAGSLVKDGVSTAKQVTEAGSVTVMDLGTLTLQTP 382

QY 484 ---ADPTSTNNIVINISSI---DGAKKAKIETKATSKNLTSGTITLLDPTGTFYENHSL 537
DB 383 SSGGETITLTNDIINIASLGGGGTSPAKLATNTASQAITIN-AVNLVDADGNAYEDPIL 441

QY 538 RNPQSDIILEKASGTVTSTAVTEDPIMGE---KEHYGVQGTWGPVIGTGTAST-TATFN 593
DB 442 ATSKPTAI---VAITNASTVQPTDNLNYPVPPHYGYQGNW-TVTMDTETATKATLUT 497

QY 594 WTKTGYPNPERIGSLVPSNLMNAFIDISLHYLMETANEGLQGGRAFACAGLSNFFHKD 653
DB 498 WEQTGYSNPERQGPLVPNTLWCAFSDLRAIQNLMDISVNGADYHRGFWVSGLANFLHKS 557

QY 654 STKTRGRFRLHSGGYVIGGNLHTCSDKILSAACQLFGRRDRDYFVAKNQGTIVYGGTLYYQ 713
DB 558 GSDTKRFRHNSAGYLVGVAKTDDIFSAACQLFGKDKDYLVSXNNANIYAGSLYYQ 617

QY 714 HNEYIYSLPCKLRPCSLSYVPTPEIPVLFSGNLSYTHTDNDLKT-----KYTTYPTVK 765
DB 618 H-----ISYSAWQNLQNTIGAEAPLVNLAQLTYCHASNDKMTNTTYAARKTYAIEIK 673

QY 766 GSWGNSFALEFGGARAPICLDESALFQYMPFMKLQFYAHQEGFKEGT-EAREFGSSR 824
DB 674 GDMGDCFGVELGATVPIQTESLLEFDMYSFELKFQLVHTHDDFKENNSDQGRYFESSN 733

QY 825 LVNIALPIGIRPKRESQCDQATYNTLTGYTVDLVRSNPDCCTTLRIISGDS--WKTFGTNL 882
DB 734 LTNLSLPIGIGKFERFANNDTASYHVTAAYASPDIVRSNPDCCTTSLVSPDSAVVTKANNL 793

QY 883 ARQALVLRAGNHFCFNSNFEAFSQSFELGRSSRNYNVDLGAKYQF 928
DB 794 ARSAFMLQAGNYLSLSHNIEIFSQGFELGRSSRTYNDLGSKIQF 839

RESULT 8
P71132
ID P71132 PRELIMINARY; PRT; 847 AA.
AC P71132;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE POMP91A.
OS Chlamydophila abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83555;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=96406378; PubMed=8810511;
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;
RT "Identification of a multigene family coding for the 90 kDa proteins of the ovine abortion subtype of Chlamydia psittaci.";
RL FEMS Microbiol. Lett. 142:277-281(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the highly immunogenic cluster of 90-kilodalton envelope proteins from the Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
DR EMBL; U65942; AAC15921.1; -;
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMs; TIGR01414; autotrans_barl; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
SQ SEQUENCE 847 AA; 90694 MW; 754C958E7F11179E CRC64;

Query Match 34.4%; Score 1641.5; DB 2; Length 847;
Best Local Similarity 38.5%; Pred. No. 2.6e-67;
Matches 376; Conservative 138; Mismatches 285; Indels 177; Gaps 25;

QY 1 MKSSPPKVFSTFATPLPSMIATE---TVLSSASFQGNKGN-PSVRESQEDAGTYLIF 56
DB 1 MKHPVYWFLLSSSLVSNSLYSEEDPQKTLTSAHNGNTNSEPFNPLSTNSNGTIYTC 60

QY 57 KGNVTLENIPTGTALTTSKCNNTKGLTFTGNGSLLFQTVDAAGTAVAGAAVNSVVDKS 116
DB 61 TGNICIAVAGLDGSLSSCSCTDTAGNLSFLNGVYLCFDNITTOSSHEGAISVSGTKT 120

QY 117 TTFIGFSSLSFTASPGSSITTKGAVSCSTGSLSTKNVLSLFSKNFSTDNGGAIKTAKIL 176
DB 121 LDISGFSLSFCAYCPPGA--TGYGAIK-AVGNTTIKDNSSLVFHKNCSTGEGGAIQCKAS 177

QY 177 SLGTTMSALLFSENSSKKGAIQTSDALITITGNQGEVFSFSDNTSSDGAIFTEASVTI 236
Db 178 S-----SEAEIKI 185
QY 237 SNNAKVSFIDNKVTVGASSSTTGDMSGGAI CAYKTSTDTKVTLTGNOMLLFSNNVTSTAGG 296
Db 186 EN-----NQLVFAENSSSSGG 203
QY 297 AIYVKLELASGGTLFSRNSVNGGTAPKGAIAIEDS-GRLSLSADSQDIFVFGNVTIS 355
Db 204 AIYADKLITVSGGTLFSNNVS-ASPKGGAICIKUSGGECSTALDGLDITFCNKIKI 262
QY 356 T---TPGTRSSIDLGTSAKWTALRSAGRAIYFDPITTTGSSSTTVTVLKVNETPADSA 412
Db 263 TNGGSPVTTRNSIDLSSGKFTKLNAKEGFGIFDYDITGGG-----DELNINK--QDT 315
QY 413 LQYTGNIIFGEKLESETEADSKNLTSKLLOPVTLSSGTLSLKHGVTLOQAFQOQADSR 472
Db 316 VDTGKLVFSGERLUSDEKKVAANLKSDFKQPLKIGSGSLILKDGVTLETKSFQTQEGAT 375
QY 473 LEMDVGTTLBP-----ADTSTINNLVINISSIDGA---KKAKIETKATSKNLTLSGTL 524
Db 376 VMVDLGTTLQTPSSGGTITLTNLDINVASLGGGVADPAKVEATTESKTVIN-AVNL 434
QY 525 LDPTGTFYENHSLRNPOSYDILELK--ASGTVTSTAV-----TPDPIMGKFFHYGQGTW 577
Db 435 VDDGNAYEYFILAASQPPFAIEVRSGSGSITKPTTNLENYTPPT-----HYGYQGNW 488
QY 578 GPIVWVGAST---TATFNMTKGYINPBERISLVPNSLWNAFIDISLHYLMETANEG 634
Db 489 -TWTWKQSSAQEKATALTWEQGYSPNPERQSLVENTLWGSFSDIRATQNLMDISVNG 547
QY 635 LQGDRAFWCAGLGNFFHKDSTKTRRGRHLSGGVIGGNLHTCSDKILSAFQOLFQDR 694
Db 548 ADVHRGFWSVGLGNFLHKSQSDTKRFRHNSAGVALGYAQTSEDVFSAPQOLFQKDK 607
QY 695 DYFAVKNQGVYGGTYLYQHNETYISLPCKLRPCSLSYVPT-----EIPVLFSG 743
Db 608 DYLVSKNSSTVYAGSIYYQH-----ISYWNWTNTLLQNTLGAEPVLNA 652
QY 744 NLSYTHDNDLTKY-----TTPYTVKSGWNSDFALEFGGRAPICLDSEALFEQYM 795
Db 653 QLAYCHASNMTKMTDTYAPPKTTYSIEIKGDWGNDCFGVEFGAKAPI-ETASLLFDMS 711
QY 796 PFMKLOFVYAHQGFKEQGT-EAREFGSSRLVNLALPIGIRFDEKSDCOQATVNTLIGYT 854
Db 712 PFVKLQLVHAHQDDFKENNSDQRYFESNLTNLNMPIGVKLEKFSKHUTASNLILAYA 771
QY 855 VDLVRNPDCITLIRISGDS--WKTFTGNLARQALVLRAGNHFCFNSNFFAFQSFELR 912
Db 772 PDIVRNPDCITSLVSPTSVAVWTKANNLARHAFILQAGNYLALTRENTLFSQFGFELR 831
QY 913 GSSRNNVDLGAQYQF 928
Db 832 GSCRTNIDLGSKIQF 847

RESULT 9

P71133
ID P71133 PRELIMINARY; PRT; 846 AA.
AC P71133;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE POM91B precursor
OS Chlamydia abortus.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.
OC NCBI_TaxID=83555;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=S26/3;
RX MEDLINE=96406378; PubMed=8810511;
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;

"Identification of a multigene family coding for the 90 kDa proteins of the ovine abortion subtype of Chlamydia psittaci.";
FEMS Microbiol. Lett. 142:277-281(1996).
[2]

SEQUENCE FROM N.A.

RC STRAIN=S26/3;
RC MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the highly immunogenic cluster of 90-kilodalton envelope proteins from the Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
DR EMBL; U65943; AAC15923.1;
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF02415; Chlamydia PMP; I.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW Signal.

FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 846 POMP91B.
SQ SEQUENCE 846 AA; 90834 MW; 4CDC31DC03C2964E CRC64;

Query Match 33.6%; Score 1604.5; DB 2; Length 846;
Best local similarity 38.7%; Pred. No. 1.3e-65;
Matches 368; Conservative 140; Mismatches 269; Indels 173; Gaps 26;

QY 23 TETVLDSSASFDGN-KGNFVSFVRESQEDAGTYYLFGNVTLNIPGTGTAITYKSCFNNTK 81
Db 26 TNETLSSSYNGNVTSDEFVKET--TSGAIVTCEGNVCI-SYAGKDSPLNKSCEFST 82
QY 82 GDLTFTGNGNSLLFQTVDACTVAGAAVNSVDKSTTFIGFS--SLSFASPGSSSITGK 139
Db 83 ENLSFIGNGYTLCFDNIITQSSHPGALSVDGNTKLDISGSLFSCAYCCPPG---TTGY 139
QY 140 GAVSCSTGSLSTKYNVSLLPKSNFSTDNAGIAITAKLTLSTLGTWTMSALFSENTSKKGAI 199
Db 140 GAIQ-TKGTTLTKDNGSLVFHKNCSAEGGAIQCK----- 173
QY 200 QTSDALITIGNQGEVFSFSDNTSSDGAIFTEASVTSINNAKVSFIDNKVTVGASSSTTGD 259
Db 174 -----SSSSTAE 180
QY 260 MSGGAI CAYKTSTDTKVTLTGNOMLLFSNNVTSTAGGAIYVKKLELASGGLTLFSRNSVN 319
Db 181 LK-----LENNKNLVFSENSKEKGAIVADKLTVSGGTLFSNNVS 224
QY 320 GGTA PKGAIAIEDS-GRLSLSADSQDIFVFGNVTST---TPGTRSSIDLGTSAKMTA 375
Db 225 HNSSPKGAICIKDSGEGCSLTANLGDITFDGNKIITNGGSPVTTRNSIDLGGGKFTK 284
QY 376 LRSAAGRAIYFVDPI-TTGSSTTVTVLKVNETPADSAQYTCGNIIFTGEKLESETEADS 434
Db 285 LNAKEGFGIFFDPIANTGGSTEI-----ELNKTESDIT--YTGI VFSGEKLSDEKTVP 338
QY 435 KNLTSKLOPVTLSSGGLTLKHGVTLOQAFQOQADSRLEMDVGTTL-----PADTSTIN 490
Db 339 ANLKS YFKQPLKTAGSLVKDGVTLLEAKKITQTKGSTVMDLGTTLQTPSSSGEITLT 398
QY 491 NLVINISSI---DGAKKAKIETKATSKNLTLSGTLTLLDPTGTFYENHSLRNPOSYDILE 547
Db 399 NLDINIASLGGGGGTAPAKLATNATSAQIASIA-AVNLVNTDSNTYEDPILSASKSPSAI- 456
QY 548 LKASGTVTSTAVTTPDIPMEKEF---HYCYOCTWGPVWGTGAST---TATFNMTKGYI 600
Db 457 ---TATSSSTVTPPETNLUKNYTPPTHYGYQGNW-TVTWKQSSAQEKATATUTWEQGY 512
QY 601 PNPERIGSLVPNSLWNAFIDISLHYLMETANEGLQGDRAFWCAGLSENFHKDSTKTRRG 660
Db 513 PNPERVGSILVPNTLWCAFSDTTRAIQNLMDISVNGADYSGFVWVSLANFLNKSQDTKRK 572
QY 661 FRHLGGYVIGNLHTCSKILSAFQOLFQDRDRYFVAKNQGVTVGGTYLYQHNETYIS 720
Db 573 FRHHSAGVALGYAQTSPSDVCSAAFCQLFGKDKDYFVSKNSSTIYAGSIYYQH----- 626

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Qy 721 LPCKLRPCSLSYVPT-----EIPVLFSGNLSYTHDNDLTKYK-----TY 761
Db 627 -----ISYWNWTNLLQNTLGAEPVLNAQLTYCHASNKNKNTMTNTYTPKNTVP 677
Qy 762 PTVKSGWNSDFALEFGGRAPICLDSEALPQYMPFMKLOFYAHQEGFKEQGT-EAREF 820
Db 678 SEIKGDWNCDFGVEFGAKAPI-ETASLLFDYMFVKQLQVLAHQDDFKNNSDQGRYF 736
Qy 821 GSSRLVNLALPIGRFDRKESDQDQATYNTLGYTVDLVRSPDCPTTLIRISGDS--WKTF 878
Db 737 ESNLNTLSMPLGVKLEKFSKDKTASYNTLAYAPDIVRSNPDCTASLLVPTSVAWYTK 796
Qy 879 GTNLARQALVLRAGNHCFNSNFAPSFQSFELRGSSRNYNVDLGAQYQF 928
Db 797 ANNLAHAFILQAGNYLALTRNTELFQGFELRGSCRTYNIDLGIQF 846

RESULT 10
Q823X5
ID Q823X5 PRELIMINARY; PRT; 1011 AA.
AC Q823X5;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN CCA00278.
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapfle E., Khouri H., Federova N.B., Carty H.A.,
RA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoi P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AB016995; AAP05029.1; -.
DR TIGR; CCA00278; -.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMS; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMS; TIGR01376; POMP_repeat; 6.
KW Complete proteome.
SQ SEQUENCE 1011 AA; 107952 MW; EBDAGFAIC46DEB6 CRC64;

Query Match 29.5%; Score 1410.5; DB 16; Length 1011;
Best Local Similarity 34.4%; Pred. No. 1.2e-56;
Matches 360; Conservative 157; Mismatches 377; Indels 151; Gaps 30;

Qy 1 MKSSFPKVFESFPAIFPLSMIA-TEVLDSSAFDGNKGNFSVRSEQEDAGTYLFGN 59
Db 1 MKASLAKFLISTLTLLFYGFQAFSLVVPNGYDGNLRETFFYTITSNPEGTTALSGN 60
Qy 60 VTLENIPTGTALTATKSCFNNTKGDLTFTGNLPGTVDAGTVAGAAVNSVVDKST-- 117
Db 61 LNLNLNDNSVATPSSCFNSAGSMITVGRNHLTF--INLRTSANGAALSIPPTTPES 118
Qy 118 ----TFTGFSLSF-----IAPGSITTG-KGAVSCSTGSLTKVNLKSNF 163
Db 119 FPTYIKGVNLTSPSNCLMARTTAPNTTTPVNPNGAFYKAPVLENIQVLPKNNR 178
Qy 164 STD-----NGGAIITA-KTSLTGTMTSALPSENTSSKK 195
Db STRAIN=LLG;

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Db 179 AADSGGLWVETAGISLNKSKMQFLSNVANGGAINASKSLDVT-QCPISILFRSNAEKL 237
Qy 196 GGAITQSDALITGNQGEVSFDNTS-----SDSGAAITFEASVTISNNAKVSFIQNK 248
Db 238 GGAIOAVDPATNTQVNTAVRESENGSVQFDANNAKSGGAIYSKGNVDFSNNAQL-LIQNN 296
Qy 249 VTGASSSTTGM--SGGAI-CAYKTSTD-----TKVTLTGOMLLFPSTNTST 292
Db 297 SASPEVANTNEVLGGGGAIFCVOQTPTQPPPPPTTNPVFSGLTITNQKILLPANNFAA 356
Qy 293 TAGGAIYVKLELASGGLTLFRSNSVNGGTAPKGAIAIEDSGELSLSDAGDIYFLGN- 351
Db 357 TAGGAIYGEKYSITSSGKMTFTNN-----IAKGGAIYIPENGELTISADYGDIMFYENL 411
Qy 352 -----TVTSTPGNRRSIDLGTSAKMTALSAAGRAIYFYDPITT-----GSSTTTVDVLK 403
Db 412 KKDDATVT-----RNAVTLAKGATIKLLAASGDHKLCFYDPIVTTLPETAPTNDKTLT 464
Qy 404 VNETPADSA--LOYTGNIIPTGEKISETEAADSKNLTSLKLOPVTLSGGLTSLKHGVTIQ 461
Db 465 INQDKTSTPTPTNYIGTLFSGAYVDSQSASTANFESTIYQKVILGGKLVADKASLS 524
Qy 462 TOAFTQADSRLEMDVGTTL-----EPADTS-----TINNVLIN 495
Db 525 VASFTQETDSILLMDNGTTLAITEHSHQTPAAGGGGGGTPTQEAETDGVISLNLHVN 584
Qy 496 ISSI-DGAKKAKIETKATSKNLTLSGTTTLLDPTGTFYENHSLRNPQ--SYDILELKASG 552
Db 585 ISSITEQEGAKLETNTDGTITLTHVSLDDVSGTAYENHDLFNKDTVTINLLSLSTAG 644
Qy 553 TVTSTAVTPD-PIMGE-KFHYGYQGTGPIVWGTGASTT-----ATENWTKTGYIPNPE 604
Db 645 DSKTTINGLDTLRGDAPQVGYQGSW-QLAWENGADANKQKILKAT--WTKTGTPTNPE 701
Qy 605 RIGSLVPSNLWNAFIDISLHYLMETANEGLQDRAFCAGLSNPFPHKDSKTKRGRFHL 664
Db 702 ROASLVPSNLWGAFFIDLSRMAALATASCDGFGYKGLWAGISNIFPHDRNSVSHGRRI 761
Qy 665 SGYVIGNLTCSDKILSAFCQLFGRDRDYFVAKNQGTVVGGLTYOHNETIYSLPCK 724
Db 762 SGYVIGANSQTVDTSVGFVAFSQIFAKSKDYVSVSSAKSAQIAGS-----AYLSVKQ 814
Qy 725 LRPCSLSYVPTIPIVLFSGNLSYTHDNDLTKYKTYPTVKSGWNSDFALEFGGRAPIC 784
Db 815 LSNITFS-----SFARINISHTNEDMKRTYTFIPEKDNWNNCWLGEIGSLPIV 866
Qy 785 LDESAL-FEQYMPFMKLOFYAHQEGFKEQGTAREFGSSRLVNLALPIGIRPDKESDQ 843
Db 867 LQITKLHLNLIIPFMNVQLGYAEHGSFKELAEARSFCSRLINLAVPVGVFKIDRSHSH 926
Qy 844 DATYNLTGYTVDLVRSPDCPTTLIRISGDSWKTGTGNLARQALVLRAGNHCFNSNFA 903
Db 927 PDFYSLAISYIPDVVWRNPGCNTLLANGVRWKTATNLRHGLLMQGSTHTTAVLSNIEI 986
Qy 904 FSGFELRGSSRNYNVDLGAQYQF 928
Db 987 FSGSCELRSRRNYNVNGSKIRF 1011

RESULT 11
Q8VU49
ID Q8VU49 PRELIMINARY; PRT; 602 AA.
AC Q8VU49;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydia psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N.A.
Db STRAIN=LLG;

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GN CCA00280.
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_TaxID=83557;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Pederoza N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoi P.M.,
Fraser C.M.;
RT "Genome sequence of Chlamydia phila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147 (2003).
DR EMBL; AE016995; AAP05031.1; -.
DR TIGR; CCA00280; -.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF02415; Chlamydia PMP; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW Complete proteome.
SQ SEQUENCE 843 AA; 90476 MW; 0B240F4687AFC7A CRC64;

Query Match 24.9%; Score 1186.5; DB 16; Length 843;
Best Local Similarity 32.7%; Pred. No. 1.7e-46;
Matches 314; Conservative 140; Mismatches 358; Indels 147; Gaps 26;

QY 1 MKSSPKF-VFSTP-AIFPLSMIAETVLDSSASFGKNN-GNFSVRSQEDAGTYLTK 57
Db 1 MKNSLYGLIFSSFTASIAFHSVNADNLASSESFDGSTGAGQFTSKQSTADAGTYT 60

QY 58 GNVLTENIPGTGTAITKSCENTKGDLTFTNGNSILFOTVDAGTVAGAAVNSVVDKST 117
Db 61 GVDVTHVKTTPANT-SCFKNSSGNLTFTGANHSLIFEDI-ISTAQGAIAISANTDAK 118

QY 118 TPIGFSSISFASPGSSITTKGAVSCSTGSLTKNVSLLFSKNSFSTNDGGAITAKT 177
Db 119 KMSGFNTLAFVAAP-QATTGAAV-YALGTTTIKENKLIIFGNHSTAAGGAIH- 170

QY 178 LTGTMSALFSENTSKKGAIQTSDALTITNQGEVFSFSDNTSDSGNAIFTEASV 237
Db 171 ----- 170

QY 238 NNAKVSFIDNKVTGASSITGDMSGGAI CAYKTSITDKVTLTGNQMLLFSNNSTTAG 297
Db 171 -----CAKTGAIEAVLTLOQNASMLFRNNSAATTGA 202

QY 298 IYVKLELASGGLTLFSRNSVNGTAPKGAIAIEDSGELSLASDGDIVFLGNTVTST 357
Db 203 IHAERFILKAGGTTLFENN-ATQKGAISAGSGEISLSADDSIIFKGNITIDA- 257

QY 358 PGTNRSS-IDLGTSAKMTALRAAGRAIYFPIPTGSSSTTVDVLKVNETADSLQYT 416
Db 258 -GNKVSNGIHVGTGNPKAKLEAKESQSILFYFV- AEGTADSNLEINK--ADGTSVT 312

QY 417 GNIIFTGKLSSTEADSKNLTSLQPVTLTSGTSLSKHGVTLOQAFQOADSRLMD 476
Db 313 GSIIIFSGRYI-ESPHKMKHV-STFQPLTLSSGLVLEKGAHLKAKSLTQTAGSKV 370

QY 477 VGTTLPEADTSTNNLVINISSIDGAKAKIETKATSKNLTLSGTTITLDPGTGFV 536
Db 371 QTSSTETKENIDIKELWLRLDDFNPTATCISTGNAHTITIKPLGVFTDQETFDN 430

QY 537 LRNPQSYDILELKASGTVSTATVPDIMEK--PHYGQCTGWPVNGT-----GA 586
Db 431 LAYSIDQEFLOL-ADKXDTIKSLIVDIPQAVRNKLDSDSHSGYQKWS-IDMKTVPG 488

QY 587 ST-----TATFNWTKTYIP---NPERIGSLVFNLSNAFIDISLHYLMETANEGL 639
Db 489 TTLGTXTATVHWPTGYIPGGQEQETTPLVNLTWNGNFSIDRLNERTVESLAVNSLC 548

QY 640 AFWCAGLSNPFHKDSTKTRGRFHLHSGGYVTGNLHTCSDKILSAAPCOLFGRDRDYFA 699
Db 549 GFMAAGIKNYLSYSPAENYVFOHNAAGYAGMKHTLSENFAAFSOLFGRDORHANG 608

QY 700 KNOGTVYGGTILYOHNETYISLP-----CKLRPCSLSVVPTPEIPVLPSGNLSYTHTD 751
Db 609 HVDHQTLSGSFYAHH---VGLPMLRFLCGSKKCPPELOASPS-IPVIVNAQLSYSHN 664

QY 752 NDLTKYTYPTVAVKSGWGNDSFALEFGGRAPICLDE-SALFEQYMPFMKLOFVYAHQGF 810
Db 665 NHLTIHEDTTKTGMSNYSALAEGLSTFVYTLKSCPSILKNVSPFVKLQGVSEQRKF 724

QY 811 KEQTEAREFGSSRUVNLALPIGIRFRDKESQDQATYNTLIGYTVDLVRSNPDCTTLRI 870
Db 725 SEGLRRLCFSTYLANLALPIGIRFRFAVDLSAMYVHDVFRIDPETWTLFLI 784

QY 871 SG-DSWTKFTGNLARQALVLRAGNHFCSNFEAFSPQSFELGRSSRNYNVDLAKYOF 928
Db 785 GGLAPWTHANNLATKAIWVSGRFAVRSNIEVPAEGNCERLSSSHSYNYDFGAKIHF 843

RESULT 14
QYVU50
ID Q8VU50 PRELIMINARY; PRT; 700 AA.
AC Q8VU50;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative polymorphic membrane protein (Fragment).
OS Chlamydia psittaci (Chlamydia phila psittaci).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_TaxID=83554;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=POS;
RA Larocau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
serotype-1 Chlamydia psittaci strains.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243415; AAL36959.1; -.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF02415; Chlamydia PMP; 1.
DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
FT NON TER 700
SQ SEQUENCE 700 AA; 74200 MW; 2C38E504AF48D1D1 CRC64;

Query Match 24.6%; Score 1175; DB 2; Length 700;
Best Local Similarity 35.5%; Pred. No. 4.6e-46;
Matches 284; Conservative 120; Mismatches 227; Indels 170; Gaps 25;

QY 23 TETVLDSSASFDGN-KGNFVSRESQEDAGTYLTKGNVTLENIPTGTATKSCFNNTK 81
Db 26 TNETLTSSDYSNGVNTSDFEVKET--TSGAIYTCGNVCI-SYAGKDSPLNKCFSFT 82

QY 82 GDLTGTGNSLLFQTVADAGTVAGAAVNSVVDKSTTFIGFSSLSFIASPGSITTKGA 141
Db 83 ENLSFTGNGYTLFCFONITTTANPAGINVGQOKILNVSGLFSCAHPGP--TTGYCA 140

QY 142 VSCSTGSLTKNVSLLFSKNSFSTNDGGAITAKTILSTLTGTTMSALFSENTSSKKGAIQT 201
Db 141 IQ-----TKGVS----- 147

QY 202 SDALITGNGEVFSFSDNTSDSGAAIFTEASVTISNNAKVDFIDNKVTCASSSTTGDMS 261
Db 148 -----TFSGNKKLIFDNNCTG-----E 165

QY 262 GGAI-CAYKTSITDKVTLTGNQMLLFSNNSTTAGGAIYVKKLELASGGLTLFSRNSVNG 320
Db 166 GGAIKCA--TGSNAELKLEGNVYVFSFGNSQKKGAIYTKLTIYADGFTLESNNVS- 222

QY 321 GTAPKGAIAIED-SGELSADSGDIVFLGNTVTSTTPGTN---RSSIDLGTSAKMTAL 376
Db 223 ASSPKGAICLDDTSSECSLTANLGDITFDGNKVIKNTNGSGSTVKRNAIDLGGSGKFTKL 282

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QY 377 RSAAGRAIYFDPI-TTGSSTTVTDVKNVETPADSALQYTGNIIFTGEKLSETEADSK 435
DB 283 NAKEGGFIHFDPIANTGSTET-----ELNKTESDTT--YTGKIVFSGEKLSEDEKTVDP 336
QY 436 NLTSKLLQPVTLSSGGLSLKHGHTLOTOAFTQAQSRLEMDVGTILE----PADTSTINN 491
DB 337 NLKSYFKQPLKIGAGSLVLKDGVTLEAKKITQKSTVVMVMDLGTTLQTPSSSGETITLTN 396
QY 492 LVINISSI---DQAKAKIETKATSKNLTLSGITITLLDPTGTFYENHSLRNPOSYDILEL 548
DB 397 LDINIASLGGGGTAPAKLATNTASQAISTA-AVNLVNTDSNTYEDPILSASKSFSAI-- 453
QY 549 KASGTVTSTAVTDPDPMGEKF-----HYGYOGTWGPIVWGTGAS---TATFNWTKTYGIP 601
DB 454 --TATTSSTSTVTPETNKNKYTPPTHYGYQGNW-TLAWPPGETWQKLTATLNWEQTYGSP 510
QY 602 NPERIGSLVNSLWNAFIDISSUHYLMETANEGLQGDRAFCWAGLSNFFHKDSTKRRGF 661
DB 511 NPERVGSVPLVTLWGSFSDIRAIQNLMDVSVNGADYSRGFWVSGLANFLNKSQDTRKF 570
QY 662 RHLSGGYVIGGNLHUCSDKILSAAPCOLFGDRDRDYFAKKNQGTGYGGLTYOHNETHYISL 721
DB 571 RHNSAGYALGVYAQTPESEDIFSAAPCOLFGKDKDYFLSKNNSSTIYAGSIYYQH----- 623
QY 722 PCKLRPCSLSY-----VPTPELVFSGNLSYTHTDNDLTKYTT-----TYP 762
DB 624 -----ISYWNQNLQNTTGAEPVLVNAQLTYCHASNMMKNTMTNTYTPKNVTPS 675
QY 763 TVKSGWGNDSFALEFGGRAP 783
DB 676 EIKGDWGSDFGVFEFGAKAPI 696

RESULT 15
Q8VU48 PRELIMINARY; PRT; 581 AA.
AC Q8VU48;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Putative polymorphic membrane protein (Fragment)
OS Chlamydia psittaci (Chlamydia psittaci)
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83554;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=POS;
RA Laroucau K., Souriau A., Rodolakis A.;
RT "Isolation of a new pmp sequence and evidence of pmp polymorphism in
RT aerotype-1 Chlamydia psittaci strains.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243419; AAL36963.1; -.
DR InterPro; IPR003369; Chlamydia_PMP.
DR Pfam; PF02415; Chlamydia_PMP; 1.
FT NON TER 1
SQ SEQUENCE 581 AA; 62860 MW; CDDF3C98522E112F CRC64;

Query Match 24.6%; Score 1172.5; DB 2; Length 581;
Best Local Similarity 40.4%; Pred. No. 4.7e-46;
Matches 253; Conservative 100; Mismatches 185; Indels 89; Gaps 17;

QY 344 GDIVFLGNTVTSSTPGN---RSSIDLGTSKMTALBSAAGRAIFYVDPI-TTGSSTTVT 399
DB 2 GDITFDGKNKIITRSSTSVKRNISISLGGGKFTKLNKAGEGFIFFDYPIANTGDTNTEI 61
QY 400 DVLKVNETPADSALQYTGNIIFTGEKLSETEADSKNLTSLKLPVTLSSGGLSLKHGVT 459
DB 62 ELNKAEE---GGSTTYTGKIVFSGEKLSDREKKVADNLKSYFTQPLKIGAGSLVLKDGVT 117
QY 460 LQTAFTQAQADSRLEMDVGTTLBPA----DTSTINNLVINISSIDGA----KKAKIETKAT 512
DB 118 LEAKKVSQTDGSTAVMDLGTTLQTSSTSGETITLTNLDINVASLGGGGVAPDPAKVEAQS 177

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QY 513 SKNLTLSGITITLLDPTGTFYENHSLRNPOSYDILELKASGTVTSTAVTPD-----PIMG 566
DB 178 GKTVITIN-AVNLVDTDGNAYEYPILATSQFTAIILAKAGSSGTTTTPTDNLKNTPTPT-- 234
QY 567 EKPHYGYOGTWGPIVWGTGAST---TATFNWTKTYGIPNPERIGSLVNSLWNAFIDISS 623
DB 235 ---HYGYQGNW-TVTKLGTSAQEETATLNWEQTYGSPNPERVGSVPLVNTLWGSFSDIRA 290
QY 624 LHYLMETANEGLQGDRAFCWAGLSNFFHKDSYKTRGRFHLSCGYVIGGNLHUCSDKILS 683
DB 291 IQNLMDVSVNGADYSRGFWVSGLANFLNKSQDTRKFRHNSAGYALGVYAQTPESEDIFS 350
QY 684 AAFCOLFGDRDRDYFAKKNQGTGYGGLTYOHNETHYISLPCKLKRPCSLSY----- 732
DB 351 AAFCOLFGKDKDYFLSKNNSSTIYAGSIYYQH-----ISYWNQNLQNT 395
QY 733 VPTEIPVLFSGNLSYTHTDNDLTKYTT-----TYPTVKGWGNDSFALEFGGRAPIC 784
DB 396 IGAEAPVLVNAQLTYCHASNMMKNTMTNTYTPKNVTPSEIKGDWGSDFGVFEFGAKAPI- 454
QY 785 LDESALFEQYMPMKLQFYVAHQEGEKGQT-EAREFGSSRLVNLALPIGIRFDKESDCQ 843
DB 455 ETASLLFDMYSPEVFKQLVHAHQDDFKBNNSDQGRYFESNNLTNLSMPIGVKLEKFSHED 514
QY 844 DATYNLTGLGYTVDLVRSNPDCTTTLRIISGDS--WKTFTGNTLAROALVLRAGNHFCFNSNF 901
DB 515 TASYNLTLAYAPDIVRSNPDCTASLLVSPTSAYVWVTKANLARHAFILOAGNYLA----- 569
QY 902 EAFSQSFELRGSSRNINVDLGAKYQF 928
DB 570 -----TYNIDLGSKIQF 581

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Search completed: August 10, 2004, 13:14:18
Job time : 50 secs

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 13:00:44 ; Search time 774 seconds
(without alignments)
16465.884 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

Sequence: 1 cgccttactagtaggt.....tggttgctaaacactttc 3000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3000	100.0	3000	3	AAA27021
2	2975.4	99.2	110000	2	AAX31990_00
3	2775.6	92.5	2787	2	AAX06820
4	2241	74.7	2241	6	ABL91193
5	546.6	18.2	2781	6	ABQ84775
6	546.6	18.2	2781	6	ABQ78033
7	546.6	18.2	2781	7	ABX99200
8	531.2	17.7	273254	3	AAC81914
9	530.2	17.7	2815	2	AAX06817
10	527	17.6	2787	6	ABL91231
11	524.6	17.5	2957	3	AAX61509
12	523	17.4	534	6	ABL91192
13	522.2	17.4	2757	2	AAX06821
14	518.4	17.3	110000	2	AAX31990_05
15	518.2	17.3	2950	3	AAA30851
16	516.6	17.2	2787	6	ABL91200
17	516.6	17.2	273254	3	AAC81914
18	515.2	17.2	2784	3	AAA30852
19	515	17.2	2787	2	AAX06822
20	514	17.1	2793	2	AAX06823
21	514	17.1	2793	6	ABL91206
22	514	17.1	2793	7	ACA30626
23	513.6	17.1	3000	3	AAA30853

24	512.6	17.1	2950	3	AAA30849	Aaa30849 Chlamydia
25	509.8	17.0	110000	2	AAX31990_05	Continuation (6 of
26	506.6	16.9	3050	3	AAA48838	Aaa48838 Chlamydia
27	506	16.9	3000	2	AAX06828	Aax06828 Chlamydia
28	503.6	16.8	2811	6	ABL91260	Ab191260 Chlamydia
29	503.6	16.8	2811	7	ACA30625	Aca30625 Prokaryot
30	496.2	16.5	110000	2	AAX31990_04	Continuation (5 of
31	491.8	16.4	2790	3	AAA30854	Aaa30854 Chlamydia
32	477	15.9	2808	3	AAA48839	Aaa48839 Chlamydia
33	469.4	15.6	2784	3	AAA30850	Aaa30850 Chlamydia
34	465.8	15.5	2787	6	ABL91241	Ab191241 Chlamydia
35	465.8	15.5	2787	7	ACA30627	Aca30627 Prokaryot
36	465.8	15.5	2950	3	AAA30847	Aaa30847 Chlamydia
37	465.8	15.5	3200	2	AAX06816	Aax06816 Chlamydia
38	435.8	14.5	2784	3	AAA30848	Aaa30848 Chlamydia
39	389	13.0	3050	3	AAZ61508	Aaz61508 DNA encod
40	378.4	12.6	2838	2	AAX06827	Aax06827 Chlamydia
41	348.8	11.6	2750	3	AAA28690	Aaa28690 C. pneumo
42	348.4	11.6	2520	6	ABQ84758	Abq84758 Chlamydia
43	348.4	11.6	2520	6	ABQ78016	Abq78016 Chlamydia
44	348.4	11.6	2520	7	ABX99183	Abx99183 C. psitta
45	345	11.5	2526	3	AAA28691	Aaa28691 C. pneumo

ALIGNMENTS

RESULT 1
AAA27021
ID AAA27021 standard; DNA; 3000 BP.
XX
AC AAA27021;
XX
DT 15-SEP-2003 (revised)
DT 11-AUG-2000 (first entry)
XX
DE Chlamydia pneumoniae 98kD putative outer membrane protein gene.
XX
KW Chlamydia; antigen; vaccine; infection; outer membrane protein; ds.
XX
OS Chlamydophila pneumoniae.
FH Key Location/Qualifiers
FT CDS 101..2887
FT /*tag= a
FT /product= "98kDa putative outer membrane protein"
XX
WO200026237-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-GB003579.
XX
PR 29-OCT-1998; 98US-0106070P.
PR 01-MAR-1999; 99US-0122066P.
PR 27-OCT-1999; 99US-00428122.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Dunn PL;
PI WPI: 2000-365569/31.
PI P-PSDB; AAY94327.
XX
DR Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for
DR vaccination and protection against Chlamydia infection.
XX
CC Claim 1; Fig 1; 93pp; English.
XX
CC The present sequence is the 98kDa putative outer membrane protein gene
CC from Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of

the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BspGI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame C-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pCA-Myc-His) by restricting both the vector and the PCR product with NotI and BamHI and performing a ligation reaction. This expression vector was injected intramuscularly and intranasally into mice, which were subsequently inoculated with Chlamydia pneumoniae. The chlamydial lung titers of the immunized mice were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protection against Chlamydia infections, especially Chlamydia pneumoniae infections. The polypeptide may also be administered orally to treat Chlamydia infection. The present sequence may also be used in the construction of attenuated Chlamydia strains that can over-express the gene or express it in a non-toxic form. (Updated on 15-SEP-2003 to standardise OS field)

Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 U; 0 Other;

Query Match 100.0%; Score 3000; DB 3; Length 3000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGCTCTTACCTAGTAGAGTTGAGTGAATTTCTTGACTTGTTCTCCTATTGGTGTACT	60
Db	1	CGCTCTTACCTAGTAGAGTTGAGTGAATTTCTTGACTTGTTCTCCTATTGGTGTACT	60
Qy	61	CTTAAATATTAATCAAAATCAAAATATATTTTCAATGAAGTCTTTTCCCAA	120
Db	61	CTTAAATATTAATCAAAATCAAAATATATTTTCAATGAAGTCTTTTCCCAA	120
Qy	121	GTTCGTATTTTACATTTGCTATTTTCCCTTTGTCTATGATGCTACGAGACATTTT	180
Db	121	GTTCGTATTTTACATTTGCTATTTTCCCTTTGTCTATGATGCTACGAGACATTTT	180
Qy	181	GGATTCAGTGGAGTTTCGATGGGAATAAAATGTAATTTTTCAGTTCGAGAGTCA	240
Db	181	GGATTCAGTGGAGTTTCGATGGGAATAAAATGTAATTTTTCAGTTCGAGAGTCA	240
Qy	241	GGAGATGCTGGATCTACTATTTTAAAGGAAATGTCATCTAGAAAATATTCCTGG	300
Db	241	GGAGATGCTGGATCTACTATTTTAAAGGAAATGTCATCTAGAAAATATTCCTGG	300
Qy	301	AACAGGACAGCAATCAGCAAAAGCTGTTTAAACACACTAAGGCGGATTTGACTTTCAC	360
Db	301	AACAGGACAGCAATCAGCAAAAGCTGTTTAAACACACTAAGGCGGATTTGACTTTCAC	360
Qy	361	AGGTAACGGGAATCTCTATTTGTTCCAAACGGTGGATGCGAGGACTGTAGCGGGCTGC	420
Db	361	AGGTAACGGGAATCTCTATTTGTTCCAAACGGTGGATGCGAGGACTGTAGCGGGCTGC	420
Qy	421	TGTTAACACAGCGTGGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGCTATCTTT	480
Db	421	TGTTAACACAGCGTGGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGCTATCTTT	480
Qy	481	TATTCGGTCTCTCGAAGTTCGATAACTACCGGCAAAAGAGCGCTGTAGCGGGCTGC	540
Db	481	TATTCGGTCTCTCGAAGTTCGATAACTACCGGCAAAAGAGCGCTGTAGCGGGCTGC	540
Qy	541	TAGCTTGAGTTTGACAAAAATGTCAGTTTGTCTTTTCAGCAAAAATCTTTTCAACGGATAA	600
Db	541	TAGCTTGAGTTTGACAAAAATGTCAGTTTGTCTTTTCAGCAAAAATCTTTTCAACGGATAA	600
Qy	601	TGGCGGTGTATCACCGCAAAAATCTTTTCATTAACAGGGACTACAATGTGACTCTGTT	660
Db	601	TGGCGGTGTATCACCGCAAAAATCTTTTCATTAACAGGGACTACAATGTGACTCTGTT	660
Qy	661	TTCTGAAAATACCTCTCTCAAGAAAGCGGAGCCATTACAGCTTCGATGCCCTTACCAAT	720
Db	661	TTCTGAAAATACCTCTCTCAAGAAAGCGGAGCCATTACAGCTTCGATGCCCTTACCAAT	720
Qy	721	TACTGGAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGAATCTGGAGCTGC	780

Db	721	TACTGGAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGAATCTGGAGCTGC	780
Qy	781	AATTTTACAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTTTATTTGACAA	840
Db	781	AATTTTACAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTTTATTTGACAA	840
Qy	841	TAAAGTCAACAGAGGAGCTCTCTCAACACGGGGATATGTCAGAGGTGCTATCTGTC	900
Db	841	TAAAGTCAACAGAGGAGCTCTCTCAACACGGGGATATGTCAGAGGTGCTATCTGTC	900
Qy	901	TTATAAACTAGTACAGATATCAAGTTCACCTCACTGAAATCAGATGTTACTCTTCAG	960
Db	901	TTATAAACTAGTACAGATATCAAGTTCACCTCACTGAAATCAGATGTTACTCTTCAG	960
Qy	961	CAACAATACATCGACCAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGCTTC	1020
Db	961	CAACAATACATCGACCAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGCTTC	1020
Qy	1021	CGAGGAGCTTACCTTATTCAGTAGAAATAGTGTCAATCGAGGTACAGCTCCTAAAGTGG	1080
Db	1021	CGAGGAGCTTACCTTATTCAGTAGAAATAGTGTCAATCGAGGTACAGCTCCTAAAGTGG	1080
Qy	1081	AGCCATAGCTATCGAAGATAGTGGGGAATTTGAGTTTATCCGCCGATAGTGGTACATTT	1140
Db	1081	AGCCATAGCTATCGAAGATAGTGGGGAATTTGAGTTTATCCGCCGATAGTGGTACATTT	1140
Qy	1141	CTTTTATAGGAATACAGTCACTTCTACTCTCGGAGCAATAGAAAGTATGACATTT	1200
Db	1141	CTTTTATAGGAATACAGTCACTTCTACTCTCGGAGCAATAGAAAGTATGACATTT	1200
Qy	1201	AGGAACGAGTGAAGATGACAGCTTTCGCTGCTGCTAGAGCCATCTACTTCTA	1260
Db	1201	AGGAACGAGTGAAGATGACAGCTTTCGCTGCTGCTAGAGCCATCTACTTCTA	1260
Qy	1261	TGATCCCATTAATACAGGATCAATCAACACAGTTACAGATGCTTAAAGTTAATAGAGAC	1320
Db	1261	TGATCCCATTAATACAGGATCAATCAACACAGTTACAGATGCTTAAAGTTAATAGAGAC	1320
Qy	1321	TCGGCAGATTTGCACTACATATACAGGGAACATCATCTTCAACAGGAGAAAGTTATC	1380
Db	1321	TCGGCAGATTTGCACTACATATACAGGGAACATCATCTTCAACAGGAGAAAGTTATC	1380
Qy	1381	AGAGACAGAGCGCGAGATTTCAAAAATCTTTCGAGCTACTACAGCTGTAAGTCT	1440
Db	1381	AGAGACAGAGCGCGAGATTTCAAAAATCTTTCGAGCTACTACAGCTGTAAGTCT	1440
Qy	1441	TTCAGAGGTACTCTATCTTTTAAACATGAGTGAATCTGAGACTCAGGCATTTCACTCA	1500
Db	1441	TTCAGAGGTACTCTATCTTTTAAACATGAGTGAATCTGAGACTCAGGCATTTCACTCA	1500
Qy	1501	ACAGGCAGATTTCTGCTCGAAATGAGCTAGGAACTACTTAGAACCTTGCTGATCTAG	1560
Db	1501	ACAGGCAGATTTCTGCTCGAAATGAGCTAGGAACTACTTAGAACCTTGCTGATCTAG	1560
Qy	1561	CACCAATAACAAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAGAGAGCAAAAT	1620
Db	1561	CACCAATAACAAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAGAGAGCAAAAT	1620
Qy	1621	AGAAACCAAGCTACGTCAAAATAATCTGACTTTATCTGAAACCATCATTATTGACCC	1680
Db	1621	AGAAACCAAGCTACGTCAAAATAATCTGACTTTATCTGAAACCATCATTATTGACCC	1680
Qy	1681	GACGGCAGCTTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCTAGCATCTTAGA	1740
Db	1681	GACGGCAGCTTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCTAGCATCTTAGA	1740
Qy	1741	GCTCAAAAGCTTCTGGAATGTAACAGCACCGCAGTACTCCAGATCTTAAATGGGTGA	1800
Db	1741	GCTCAAAAGCTTCTGGAATGTAACAGCACCGCAGTACTCCAGATCTTAAATGGGTGA	1800
Qy	1801	GAATTTCCATTAACGGCTATCAGGAACTTTGGGCGCCAAATTTGTTGGGGAGCAGGGCTTC	1860

Db 1801 GAAATTCATTACGGCTATCAGGGAACCTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC 1860

QY 1861 TAGACCTGCAACCTTCAACTGGACTAAACTGCGTATATTCCTTAATCCCGAGCGTATCGG 1920

Db 1861 TAGACCTGCAACCTTCAACTGGACTAAACTGCGTATATTCCTTAATCCCGAGCGTATCGG 1920

QY 1921 CTCTTTAGTCCCTTAATAGCTTTATGGTAATGCATTTATAGATATTAGCTCTCTCCATTATCT 1980

Db 1921 CTCTTTAGTCCCTTAATAGCTTTATGGTAATGCATTTATAGATATTAGCTCTCTCCATTATCT 1980

QY 1981 TATGGAGACTGCAAAACGAGGGTTGACAGGAGACCGTGTCTTTTGGTGTCTCGATTATC 2040

Db 1981 TATGGAGACTGCAAAACGAGGGTTGACAGGAGACCGTGTCTTTTGGTGTCTCGATTATC 2040

QY 2041 TAACCTTCTTCATAGAGATAGTACAAAACACAGACGGGGTTTGGCCATTGAGTGGCGG 2100

Db 2041 TAACCTTCTTCATAGAGATAGTACAAAACACAGACGGGGTTTGGCCATTGAGTGGCGG 2100

QY 2101 TTATGTCTATAGGAGGAAACCTACATCTCTTTCAGATAAGATTCTTAGTCTGCTCATTTTG 2160

Db 2101 TTATGTCTATAGGAGGAAACCTACATCTCTTTCAGATAAGATTCTTAGTCTGCTCATTTTG 2160

QY 2161 TCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTCTACGG 2220

Db 2161 TCAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTCTACGG 2220

QY 2221 AGGAACCTCTATATACAGCACAGCAACGAACTATATCTCTTCTTGGCAAACTACGGCC 2280

Db 2221 AGGAACCTCTATATACAGCACAGCAACGAACTATATCTCTTCTTGGCAAACTACGGCC 2280

QY 2281 TTGTTGCTTCTATGTTCTTACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA 2340

Db 2281 TTGTTGCTTCTATGTTCTTACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA 2340

QY 2341 CACCCATACGGATACGATCTGAAACCAAGTATACAAATATCTACTCTGTTAAAGGAAG 2400

Db 2341 CACCCATACGGATACGATCTGAAACCAAGTATACAAATATCTACTCTGTTAAAGGAAG 2400

QY 2401 CTGGGGGAATGATAGTTTGGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTAGATGA 2460

Db 2401 CTGGGGGAATGATAGTTTGGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTAGATGA 2460

QY 2461 AAGTGTCTATTTGAGCAGTACATGCCCTTCATGAATTCAGTTTGTCTATGCACATCA 2520

Db 2461 AAGTGTCTATTTGAGCAGTACATGCCCTTCATGAATTCAGTTTGTCTATGCACATCA 2520

QY 2521 GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGTCTTTGTGAA 2580

Db 2521 GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGTCTTTGTGAA 2580

QY 2581 TCTTGCTTACCTATCGGATCCGATTTGATAGGATCAGACTGCCAAGATCGAACGTA 2640

Db 2581 TCTTGCTTACCTATCGGATCCGATTTGATAGGATCAGACTGCCAAGATCGAACGTA 2640

QY 2641 CAATCTAATCTTTGGTTATCTGGATCTTGTTCGTAGTAAACCCGACTGTACGACAAC 2700

Db 2641 CAATCTAATCTTTGGTTATCTGGATCTTGTTCGTAGTAAACCCGACTGTACGACAAC 2700

QY 2701 ACTCGGAATAGCGGTGATTTCTGGAAAACTTCGGTACGAAATTTGGCAAGACAAAGCTTT 2760

Db 2701 ACTCGGAATAGCGGTGATTTCTGGAAAACTTCGGTACGAAATTTGGCAAGACAAAGCTTT 2760

QY 2761 AGTCCTTCGTCAGGGAACCAATTTTGTCTTAACTCAAAATTTTGAAGCCCTTAGCCAAAT 2820

Db 2761 AGTCCTTCGTCAGGGAACCAATTTTGTCTTAACTCAAAATTTTGAAGCCCTTAGCCAAAT 2820

QY 2821 TTCTTTTGAATTCGTTGGGTCTCTCCAAATTCAAATGTAGACTTAGAGCAAAAATACCA 2880

Db 2821 TTCTTTTGAATTCGTTGGGTCTCTCCAAATTCAAATGTAGACTTAGAGCAAAAATACCA 2880

QY 2881 ATTCTAATGCTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAGAGCTTTTAAAG 2940

Db 2881 ATTCTAATGCTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAGAGCTTTTAAAG 2940

QY 2941 ATTCTTGAAGGCTCTTTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTC 3000

Db 2941 ATTCTTGAAGGCTCTTTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTC 3000

RESULT 2

WP Sequence split into 13 fragments LOCUS AAX91990 Accession Aax91990

WP Fragment Name Begin End

WP AAX91990_00 1 110000

WP AAX91990_01 100001 210000

WP AAX91990_02 200001 310000

WP AAX91990_03 300001 410000

WP AAX91990_04 400001 510000

WP AAX91990_05 500001 610000

WP AAX91990_06 600001 710000

WP AAX91990_07 700001 810000

WP AAX91990_08 800001 910000

WP AAX91990_09 900001 1010000

WP AAX91990_10 1000001 1110000

WP AAX91990_11 1100001 1210000

WP AAX91990_12 1200001 1230025

ID AAX91990 standard; DNA; 1230025 BP.

XX AC

XX AAX91990;

XX 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX

DE Nucleotide sequence of the complete genome of Chlamydia pneumoniae.

XX

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

KW neutralising epitope; ss.

XX

XX Chlamydothila pneumoniae.

XX

PN WO9927105-A2.

XX

PD 03-JUN-1999.

XX

PF 20-NOV-1998; 98WO-IB001890.

XX

PR 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.

XX

PA (GEST) GENSET.

XX

PI Griffais R;

XX

DR WPI; 1999-357842/30.

XX

PT Genome sequence of Chlamydia pneumoniae.

XX

PS Claim 1; Page 291-611; 1912pp; English.

XX

CC The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAX34584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotide sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 1230025 BP; 367213A; 249833C; 249013G; 363589T; 0U; 3770ther;

Query Match 99.2%; Score 2975.4; DB 2; Length 110000;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2998; Conservative 0; Mismatches 1; Indels 2; Gaps 2;			
Qy	1	CGCTCTTACCTAGTAGAGGTTGAGTGAATTTCTTGACTTGTTTCTCTCTATTTGGTGATCT	60
Db	31658	CGCTCTTACCTAGTAGAGGTTGAGTGAATTTCTTGACTTGTTTCTCTCTATTTGGTGATCT	31717
Qy	61	CTTAAATATATAATTCAAAATCAAGATATATATTTTACAATGAAGTCTTCTTCCCAA	120
Db	31718	CTTAAATATATAATTCAAAATCAAGATATATATTTTACAATGAAGTCTTCTTCCCAA	31777
Qy	121	GTITGTATTTTCTACATTTCTATTTCCCTTTTGTCTATGATTTCTACCGAGACAGTTTT	180
Db	31778	GTITGTATTTTCTACATTTCTATTTCCCTTTTGTCTATGATTTCTACCGAGACAGTTTT	31837
Qy	181	GGATTCAGTTCGAGTTTCGATGGGAATAAAAATGGTAATTTTTTCAGTTTCGTGAGAGTCA	240
Db	31838	GGATTCAGTTCGAGTTTCGATGGGAATAAAAATGGTAATTTTTTCAGTTTCGTGAGAGTCA	31897
Qy	241	GGAAATGCTGGAACTACCTACCTATTTAAGGGAATGTCACTAGAAAATATTCCTCG	300
Db	31898	GGAAATGCTGGAACTACCTATTTAAGGGAATGTCACTAGAAAATATTCCTCG	31957
Qy	301	AACAGGCACAGCAATCAAAAAAGCTGTTTTAAACAACACTAAGGGCGATTTGACTTTCAC	360
Db	31958	AACAGGCACAGCAATCAAAAAAGCTGTTTTAAACAACACTAAGGGCGATTTGACTTTCAC	32017
Qy	361	AGTTACGGGAATCTCTATTTGTTCCAAAAGGTGGATGCGAGGACGTAGCAGGGCTCG	420
Db	32018	AGTTACGGGAATCTCTATTTGTTCCAAAAGGTGGATGCGAGGACGTAGCAGGGCTCG	32077
Qy	421	TGTTAAACAGCAGCGTGTAGATAAAATCTACACAGTTTTATAGGGTTTTCTTCGCTATCTTT	480
Db	32078	TGTTAAACAGCAGCGTGTAGATAAAATCTACACAGTTTTATAGGGTTTTCTTCGCTATCTTT	32137
Qy	481	TATTCGCTCTCTGGAAAGTTCGATACTACCGCAAGAGGCCGTAGCTGCTCTAGGG	540
Db	32138	TATTCGCTCTCTGGAAAGTTCGATACTACCGCAAGAGGCCGTAGCTGCTCTAGGG	32197
Qy	541	TAGCTTCAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAA	600
Db	32198	TAGCTTCAGTTTGAC-AAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAA	32256
Qy	601	TGGCGGTGCTATCACCGCAAAAACTTTTCAATTAACAGGACCTACAATGTCAGCTCTGTT	660
Db	32257	TGGCGGTGCTATCACCGCAAAAACTTTTCAATTAACAGGACCTACAATGTCAGCTCTGTT	32316
Qy	661	TTCTGAAATACCTCTCAAGAAAGCGGAGCCATTCAGACTTCGGATCCGCTTACCAT	720
Db	32317	TTCTGAAATACCTCTCAAGAAAGCGGAGCCATTCAGACTTCGGATCCGCTTACCAT	32376
Qy	721	TACTGGAAACCAAGGGAGTCTCTTTTCTGACAACTACTTTTCGGATTTCTGGAGCTGC	780
Db	32377	TACTGGAAACCAAGGGAGTCTCTTTTCTGACAACTACTTTTCGGATTTCTGGAGCTGC	32436
Qy	781	AATTTTTACAGAGCCTCGGTGACTATTTCTAATAATGCTAAAAGTTTCTTTATTCACAA	840
Db	32437	AATTTTTACAGAGCCTCGGTGACTATTTCTAATAATGCTAAAAGTTTCTTTTATTCACAA	32496
Qy	841	TAAGTTCACAGGACGAGCTCTCAACAAAGGGGATATGTCAGGAGGTGCTATCTGTGC	900
Db	32497	TAAGTTCACAGGACGAGCTCTCAACAAAGGGGATATGTCAGGAGGTGCTATCTGTGC	32556
Qy	901	TTATAAACTAGTACAGATCTAAGTTCACCTCACTCGGAAATCAGATGTTACTTTCAG	960
Db	32557	TTATAAACTAGTACAGATCTAAGTTCACCTCACTCGGAAATCAGATGTTACTTTCAG	32616
Qy	961	CAACAAATACATCGAACACAGCGGAGGAGCTATCTATGTCAAAAAGCTCGAACTGCTTC	1020
Db	32617	CAACAAATACATCGAACACAGCGGAGGAGCTATCTATGTCAAAAAGCTCGAACTGCTTC	32676
Qy	1021	CGGAGGACTTACCTTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG	1080
Db	32677	CGGAGGACTTACCTTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG	32736
Qy	1081	AGCCATAGCTATCGAAGATAGTGGGGAATTCAGTTTATCCCGCATAGTGTGTGACATTTGT	1140
Db	32737	AGCCATAGCTATCGAAGATAGTGGGGAATTCAGTTTATCCCGCATAGTGTGTGACATTTGT	32796
Qy	1141	CTTTTATGGGAATACAGTCACTTCTACTACTCTCGGACGAATAGAACTAGTATTCGACTT	1200
Db	32797	CTTTTATGGGAATACAGTCACTTCTACTACTCTCGGACGAATAGAACTAGTATTCGACTT	32856
Qy	1201	AGGAACGAGTGCAAAGATGACAGCTTTTGCCTTCTGCTGCTGGTAGAGCAATCTACTTCTA	1260
Db	32857	AGGAACGAGTGCAAAGATGACAGCTTTTGCCTTCTGCTGCTGGTAGAGCAATCTACTTCTA	32916
Qy	1261	TGATCCCATACTACAGGATCATCCACAACTTTTCAAGAGTCTTTAAAGATTAATAGAGAC	1320
Db	32917	TGATCCCATACTACAGGATCATCCACAACTTTTCAAGAGTCTTTAAAGATTAATAGAGAC	32976
Qy	1321	TCGGCAGATTTCTGCACCTACAATATACAGGGAAATCATCTTTTCACAGAGAAAAAGTTATC	1380
Db	32977	TCGGCAGATTTCTGCACCTACAATATACAGGGAAATCATCTTTTCACAGAGAAAAAGTTATC	33036
Qy	1381	AGAGACAGAGCGCGAGATTTCTAAAATCTTTAATTCTTCTGAGAGTACTACAGCTGTAACTCT	1440
Db	33037	AGAGACAGAGCGCGAGATTTCTAAAATCTTTAATTCTTCTGAGAGTACTACAGCTGTAACTCT	33096
Qy	1441	TTTCAGAGGTACTCTATCTTTTAAAACATGGAGTGACTCTGCAGACTCAGGCAATTCACCTCA	1500
Db	33097	TTTCAGAGGTACTCTATCTTTTAAAACATGGAGTGACTCTGCAGACTCAGGCAATTCACCTCA	33156
Qy	1501	ACAGCAGATTTCTGCTCTCGAAATGGAGTATCTCTAGAACTCTGTAATCTAGTAG	1560
Db	33157	ACAGCAGATTTCTGCTCTCGAAATGGAGTATCTCTAGAACTCTGTAATCTAGTAG	33216
Qy	1561	CACCATTAACAATTTGGTTCATTAACTCAGTTCTTATAGACGGTCAAGAGGCAAAAAT	1620
Db	33217	CACCATTAACAATTTGGTTCATTAACTCAGTTCTTATAGACGGTCAAGAGGCAAAAAT	33276
Qy	1621	AGAAACCAAAAGTACGTCAAAAATCTGACTTTATCTGAAACCATCACTTTTATGGACCC	1680
Db	33277	AGAAACCAAAAGTACGTCAAAAATCTGACTTTATCTGAAACCATCACTTTTATGGACCC	33336
Qy	1681	GACGGCAGCTTTTATGAAAAATCATAGTTTAAAGAAATCCTCAGTCTCTACGACATCTTAGA	1740
Db	33337	GACGGCAGCTTTTATGAAAAATCATAGTTTAAAGAAATCCTCAGTCTCTACGACATCTTAGA	33396
Qy	1741	GCTCAAAAGCTTCGGAACTGTAAACAGCACCGCAGTGTACTCCAGATCTCTATAATGGGTGA	1800
Db	33397	GCTCAAAAGCTTCGGAACTGTAAACAGCACCGCAGTGTACTCCAGATCTCTATAATGGGTGA	33456
Qy	1801	GAATTCCTATTACGGCTATCAGGGAACTTGGGGGCCAAATTTGTTGGGGGACAGGGGCTTC	1860
Db	33457	GAATTCCTATTACGGCTATCAGGGAACTTGGGGGCCAAATTTGTTGGGGGACAGGGGCTTC	33516
Qy	1861	TACGACTGCACCTTCAACTGAGCTTAAACCTGGCTATATCTCTAATCCGAGCGTATCGG	1920

Qy	401	GGGACTGTAGAGGGGTGCTGTGTAAACAGCAGCGTGTGTAGATAAAATCTACCAAGTTTATA	460
Db	301	GGGACTGTAGCAGGGGTGCTGTGTAAACAGCAGCGTGTGTAGATAAAATCTACCAAGTTTATA	360
Qy	461	GGGTTTTCTTCGCTATCTTTTATTGCGTCTCTCGGAAGTTTCGATAAATCTACCGCAAGGA	520
Db	361	GGGTTTTCTTCGCTATCTTTTATTGCGTCTCTCGGAAGTTTCGATAAATCTACCGCAAGGA	420
Qy	521	GCCGTTAGTCTCTCTACGGGTAGCTTCAGTTTGTACAAAATGTCAGTTTGTCTCTTCAGC	580
Db	421	GCCGTTAGTCTCTCTACGGGTAGCTTCAGTTTGTACAAAATGTCAGTTTGTCTCTTCAGC	480
Qy	581	AAAAACTTTTCAACCGGATAATFGCGGTGCTATACCGCAAAAATCTTTTCAATTAACAGGG	640
Db	481	AAAAACTTTTCAACCGGATAATFGCGGTGCTATACCGCAAAAATCTTTTCAATTAACAGGG	540
Qy	641	ACTACAATGTCAGCTCTGTTTTCTGAAAATACCTTCCTCAAGAAGCGGAGCCATTACG	700
Db	541	ACTACAATGTCAGCTCTGTTTTCTGAAAATACCTTCCTCAAGAAGCGGAGCCATTACG	600
Qy	701	ACTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTCTGCAAAATCT	760
Db	601	ACTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTCTGCAAAATCT	660
Qy	761	TCTTCGGATTCGAGCTGCAATTTTTATCAGAAGCTTCGGTGAATATTTCTAAATGCT	820
Db	661	TCTTCGGATTCGAGCTGCAATTTTTATCAGAAGCTTCGGTGAATATTTCTAAATGCT	720
Qy	821	AAAGTTTCTTTATTGACAATAAGGTCACAGAGCGGAGCTCTCAACAAACGGGGGATATG	880
Db	721	AAAGTTTCTTTATTGACAATAAGGTCACAGAGCGGAGCTCTCAACAAACGGGGGATATG	780
Qy	881	TCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACCTAAGGTCACCCCTCACTGGA	940
Db	781	TCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACCTAAGGTCACCCCTCACTGGA	840
Qy	941	AATCAGATGTTACTCTTCAGCAACAATAATCATCGCAACAGCGGGAGGAGCTATCTATGT	1000
Db	841	AATCAGATGTTACTCTTCAGCAACAATAATCATCGCAACAGCGGGAGGAGCTATCTATGT	900
Qy	1001	AAAAAGCTCGAAGCTCGGCTTCGGAGGACTTACCTTATTCAGTAGAATAGTGTCAATGGA	1060
Db	901	AAAAAGCTCGAAGCTCGGCTTCGGAGGACTTACCTTATTCAGTAGAATAGTGTCAATGGA	960
Qy	1061	GGTACAGCTCTTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCC	1120
Db	961	GGTACAGCTCTTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCC	1020
Qy	1121	GCCGATAGTGGTGACATTTCTTTTTAGGGAATACAGTCATTTACTCTCTGGGACG	1180
Db	1021	GCCGATAGTGGTGACATTTCTTTTTAGGGAATACAGTCATTTACTCTCTGGGACG	1080
Qy	1181	AATAGAAGTAGTATCGACTTAGGAACGAGTGGAAAGATGACAGCTTCTGCTGCT	1240
Db	1081	AATAGAAGTAGTATCGACTTAGGAACGAGTGGAAAGATGACAGCTTCTGCTGCT	1140
Qy	1241	GGTAGAGCCATCTACTCTATGATCCCATACCTACAGGATCATCCACAACAGTGTACAGAT	1300
Db	1141	GGTAGAGCCATCTACTCTATGATCCCATACCTACAGGATCATCCACAACAGTGTACAGAT	1200
Qy	1301	GTCTTTAAAAGTTAATGAGCTCCGGCAGATTCGCACTACAAATATACAGGGGAACATCATC	1360
Db	1201	GTCTTTAAAAGTTAATGAGCTCCGGCAGATTCGCACTACAAATATACAGGGGAACATCATC	1260
Qy	1361	TTTCAAGGAGAAAAGTTATCAGAGACAGGGCCGAGATTCTTAAAAATCTTACTTCGAAG	1420
Db	1261	TTTCAAGGAGAAAAGTTATCAGAGACAGGGCCGAGATTCTTAAAAATCTTACTTCGAAG	1320
Qy	1421	CTACTACAGCCTGTAACTCTTTTACAGAGTACTCTATCTTTTAAAAATGAGTACTCTG	1480
Db	1321	CTACTACAGCCTGTAACTCTTTTACAGAGTACTCTATCTTTTAAAAATGAGTACTCTG	1380
Qy	1481	CAGACTTCAGGCATTCATCTCAACAGGCAGATTTCTCGTCTCGAAATGGACGTAGGAATCTACT	1540

Db 2461 GGAAGTAGCGCTTCTGTGAATCTTGCTTACCTATCGGGATCCGATTTGATAGGAATCA 2520
 QY 2621 GACTGCCAGATGCAACGCTACAACTCTCTGGTTTATCTGTGGATCTGTGTTCTGTAGT 2680
 Db 2521 GACTGCCAGATGCAACGCTACAACTCTCTGGTTTATCTGTGGATCTGTGTTCTGTAGT 2580
 QY 2681 AACCCGACTGTACGACACACCTGCGAATTAGCGGTGATCTTTGGAAAACCTTTCGGTACG 2740
 Db 2581 AACCCGACTGTACGACACACCTGCGAATTAGCGGTGATCTTTGGAAAACCTTTCGGTACG 2640
 QY 2741 AATTGGCAAGCAAGCTTTAGTCTTTTCGTCGAGGAAACCAATTTTTCCTTTAACTCAAAAT 2800
 Db 2641 AATTGGCAAGCAAGCTTTAGTCTTTTCGTCGAGGAAACCAATTTTTCCTTTAACTCAAAAT 2700
 QY 2801 TTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGTTGGTTCATCTCGCAATTAACAATGTA 2860
 Db 2701 TTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGTTGGTTCATCTCGCAATTAACAATGTA 2760
 QY 2861 GACTTAGGAGCAAAATACCAATTTCTAA 2887
 Db 2761 GACTTAGGAGCAAAATACCAATTTCTAA 2787

RESULT 4

ABL91193

ID ABL91193 standard; DNA; 2241 BP.

XX ABL91193;

AC ABL91193;

XX 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)

XX Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

DE Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

XX Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

KW Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

KW Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

KW Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

KW Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

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KW Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

KW Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

PS Claim 5; Page 50; 364pp; English.
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed DNA which encodes a Chlamydia pneumoniae protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 2241 BP; 660 A; 475 C; 478 G; 628 T; 0 U; 0 Other;

Query Match 74.7%; Score 2241; DB 6; Length 2241;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 647 ATGTCAGCTCTGTTTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTCAGACTTC 706
 Db 1 ATGTCAGCTCTGTTTCTGAAATACCTCTCTCAAGAAAGCGGAGCCATTCAGACTTC 60
 QY 707 GATGCCCTTACCATTACTGGAACCAAGGGAAGTCTCTTTTCTGACAATCTCTTCG 765
 Db 61 GATGCCCTTACCATTACTGGAACCAAGGGAAGTCTCTTTTCTGACAATCTCTTCG 120
 QY 767 GATCTGGAGCTGCAATTTTACAGAGCTCGGTGACTATTTCTAATAATGCTAAAGTT 826
 Db 121 GATCTGGAGCTGCAATTTTACAGAGCTCGGTGACTATTTCTAATAATGCTAAAGTT 180
 QY 827 TCCTTTATTGACAAATAGGTCACAGAGCGGAGCTCTCTCAACACGGGGGATGTCAGGA 886
 Db 181 TCCTTTATTGACAAATAGGTCACAGAGCGGAGCTCTCTCAACACGGGGGATGTCAGGA 240
 QY 887 GGTGCTATCTGTCTTATAAACTAGTACAGATACTAAAGTCACTCCCTCACTGAAATCAG 946
 Db 241 GGTGCTATCTGTCTTATAAACTAGTACAGATACTAAAGTCACTCCCTCACTGAAATCAG 300
 QY 947 ATGTTACTCTTACAGCAACAATATACGACAAACAGCGGAGAGCTATCTATGTGAAAAG 1006
 Db 301 ATGTTACTCTTACAGCAACAATATACGACAAACAGCGGAGAGCTATCTATGTGAAAAG 360
 QY 1007 CTCGAACTGGCTTCCGGAGGACTTACCCTATTTCAGTAGAATAGTGTCAATGGAGGTACA 1066
 Db 361 CTCGAACTGGCTTCCGGAGGACTTACCCTATTTCAGTAGAATAGTGTCAATGGAGGTACA 420
 QY 1067 GCTCCTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCCGCCGAT 1126
 Db 421 GCTCCTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCCGCCGAT 480
 QY 1127 AGTGGTGACATTTCTTTTATAGGAAATACAGTCACTTCTACTCTCTCGGAGCAATAGTA 1186
 Db 481 AGTGGTGACATTTCTTTTATAGGAAATACAGTCACTTCTACTCTCTCGGAGCAATAGTA 540
 QY 1187 AGTAGTATCGACTTAGGAACGAGTGCAGAGATCAGAGCTTTGCTGCTGCTGGTAGA 1246
 Db 541 AGTAGTATCGACTTAGGAACGAGTGCAGAGATCAGAGCTTTGCTGCTGCTGGTAGA 600
 QY 1247 GCCATCTTCTATGATCCATAAATACAGGATCATCCAAACAGTTACAGATGCTCTTA 1306
 Db 601 GCCATCTTCTATGATCCATAAATACAGGATCATCCAAACAGTTACAGATGCTCTTA 660
 QY 1307 AAGATTAAAGACTCCGGCAGATTTCTGACTCAATATACAGGAAACATCATCTTCCACA 1366
 Db 661 AAGATTAAAGACTCCGGCAGATTTCTGACTCAATATACAGGAAACATCATCTTCCACA 720

Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes.

QY 1367 GGAGAAAAGTTATCAGAGACAGAGCCGAGATTCCTAAATACTTTACTTCGAAGCTACTA 1426
Db 721 GGAGAAAAGTTATCAGAGACAGAGCCGAGATTCCTAAATACTTTACTTCGAAGCTACTA 780
QY 1427 GAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAACATCGGAGTGACTCTGCAGACT 1486
Db 781 GAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAACATCGGAGTGACTCTGCAGACT 840
QY 1487 CAGGCATTCACTCAACAGCCAGATTCCTGCTCGAAATCGAGTGAAGTACTCTAGAA 1546
Db 841 CAGGCATTCACTCAACAGCCAGATTCCTGCTCGAAATCGAGTGAAGTACTCTAGAA 900
QY 1547 CCGTCTGATPACTAGCACCATAAACAATTTGGTCATTAAACATCAGTTCTATAGACGGTGCA 1606
Db 901 CCGTCTGATPACTAGCACCATAAACAATTTGGTCATTAAACATCAGTTCTATAGACGGTGCA 960
QY 1607 AAGAGGGCAAAATAGAACCAAGCTAGCTCAAAAATCTGACTTTATCTGGAACCATC 1666
Db 961 AAGAGGGCAAAATAGAACCAAGCTAGCTCAAAAATCTGACTTTATCTGGAACCATC 1020
QY 1667 ACTTTATTGGACCCGACGGGCAAGTTTATGAAATCATAGTTTAAAGAAATCTCAGTCC 1726
Db 1021 ACTTTATTGGACCCGACGGGCAAGTTTATGAAATCATAGTTTAAAGAAATCTCAGTCC 1080
QY 1727 TAGCACATCTTAGAGCTCAAGCTTCTGGAATCTGAACTGTAACAGCACCGCAGTGACTCCAGAT 1786
Db 1081 TAGCACATCTTAGAGCTCAAGCTTCTGGAATCTGAACTGTAACAGCACCGCAGTGACTCCAGAT 1140
QY 1787 CCTAATAAGGGTGAGAAATTCATACGGCTATCAGGAACTTGGGGCCCAATTTGTTGG 1846
Db 1141 CCTAATAAGGGTGAGAAATTCATACGGCTATCAGGAACTTGGGGCCCAATTTGTTGG 1200
QY 1847 GGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTTAAACCTGGCTATATCTCTAAT 1906
Db 1201 GGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTTAAACCTGGCTATATCTCTAAT 1260
QY 1907 CCGGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGC 1966
Db 1261 CCGGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGC 1320
QY 1967 TCTCTCCATATCTTATGAGACTGCAACGAGGAGGTTGCGGGAGACCGCTCTTTTGG 2026
Db 1321 TCTCTCCATATCTTATGAGACTGCAACGAGGAGGTTGCGGGAGACCGCTCTTTTGG 1380
QY 2027 TGTCTGGAATTAATACTTCTTCCATAGGATAGTACAAAACACGACGCGGGTTTCGC 2086
Db 1381 TGTCTGGAATTAATACTTCTTCCATAGGATAGTACAAAACACGACGCGGGTTTCGC 1440
QY 2087 CATTTGAGTGGCGTTATGTCTAGAGGAAACCTACATACCTTGTTCAGATTAAGATTCTT 2146
Db 1441 CATTTGAGTGGCGTTATGTCTAGAGGAAACCTACATACCTTGTTCAGATTAAGATTCTT 1500
QY 2147 AGTGTCTGATTTTGTTCAGCTCTTTGGAAGATAGAGACTACTTTGTAGCTAAGATCAA 2206
Db 1501 AGTGTCTGATTTTGTTCAGCTCTTTGGAAGATAGAGACTACTTTGTAGCTAAGATCAA 1560
QY 2207 GGTACAGTCTACGGAGAACTCTCTATTACAGCACAAACGAAACCTATATCTCTCTCTCT 2266
Db 1561 GGTACAGTCTACGGAGAACTCTCTATTACAGCACAAACGAAACCTATATCTCTCTCTCT 1620
QY 2267 TGCAAACTACGGCCTTGTCTGTTGTTCTTATGTTCTTACAGATTCCTGTTCTCTTTTCA 2326
Db 1621 TGCAAACTACGGCCTTGTCTGTTGTTCTTATGTTCTTACAGATTCCTGTTCTCTTTTCA 1680
QY 2327 GGAAACCTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATACACATATCTCT 2386
Db 1681 GGAAACCTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATACACATATCTCT 1740
QY 2387 ACTGTTAAAGAACTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCG 2446
Db 1741 ACTGTTAAAGAACTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCG 1800

QY 2447 ATTCTCTAGATGAAAGTGTCTCTATTGAGCAGTACATGCCCTTCATGAAATTCGAGTTT 2506
Db 1801 ATTCTCTAGATGAAAGTGTCTCTATTGAGCAGTACATGCCCTTCATGAAATTCGAGTTT 1860
QY 2507 GTCTATGCACATCAGAAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTCGAAGT 2566
Db 1861 GTCTATGCACATCAGAAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTCGAAGT 1920
QY 2567 AGCCCTCTTGTGAATCTTGGCTTACTCTATCGGGATCCGATTTGATAAGGAATCAGACTGC 2626
Db 1921 AGCCCTCTTGTGAATCTTGGCTTACTCTATCGGGATCCGATTTGATAAGGAATCAGACTGC 1980
QY 2627 CAAGATGCAACGTACAATCTACTCTTGGTTATATCTGTGGATCTTGTTCGTAGTAACCCC 2686
Db 1981 CAAGATGCAACGTACAATCTACTCTTGGTTATATCTGTGGATCTTGTTCGTAGTAACCCC 2040
QY 2687 GACTCTAGACAACTCGAATTAGCGGTGATTTCTTGAAACCTTCGGTACGAATTTG 2746
Db 2041 GACTCTAGACAACTCGAATTAGCGGTGATTTCTTGAAACCTTCGGTACGAATTTG 2100
QY 2747 GCAAGACAAGCTTTTAGTCTCTCGTGCAGGAAACCAATTTTGTCTTAACTCAAATTTTGA 2806
Db 2101 GCAAGACAAGCTTTTAGTCTCTCGTGCAGGAAACCAATTTTGTCTTAACTCAAATTTTGA 2160
QY 2807 GCCTTTAGCCAAATTTCTTTTGAATTTGGTGGTCACTCGCAATTAAGATGTAGACTTA 2866
Db 2161 GCCTTTAGCCAAATTTCTTTTGAATTTGGTGGTCACTCGCAATTAAGATGTAGACTTA 2220
QY 2867 GGAGCAAAATACCAATTTCTAA 2887
Db 2221 GGAGCAAAATACCAATTTCTAA 2241
RESULT 5
AB084775
ID AB084775 standard; DNA; 2781 BP.
XX
AC AB084775;
XX
DT 29-AUG-2003 (revised)
DT 25-FEB-2003 (first entry)
XX
DE Chlamydia psittaci antigen CP4#12 encoding DNA SEQ ID NO:56.
KW Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
KW immunisation; antibacterial; infection; gene; ds.
XX
OS Chlamydophila caviae.
XX
FH Key Location/Qualifiers
FT CDS 1..2781
FT /tag= a
FT /product= "antigen CP4#12"
FT
XX
PN WO200253588-A2.
XX
PD 11-JUL-2002.
XX
PF 17-DEC-2001; 2001WO-US048715.
XX
PR 15-DEC-2000; 2000US-00738269.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
XX
DR WPI: 2002-537942/57.
DR P-PSDB; ABP56019.
XX
PT Vaccine for immunization of animal, preferably bovine, against Chlamydia
PT psittaci, comprises at least one polynucleotide having a C. psittaci
PT sequence, or at least one C. psittaci antigen.

Db 2115 TGTATATTATCAGCATGTGAGCAAGTTTGATGATCTCAGCGGGTATTATTTAATGGCCCTAA 2174
QY 2281 TTGTTTCGTTGCTTATGTTCTTACAGAGATTCTCTGTTCTCTTTTCAGGAAACCTTTAGCTA 2340
Db 2175 CACGTGTTGTTACAGGGTTTCTAAGAGATTCCTATTTTCTGGATGACAAATTACCTA 2234
QY 2341 CACCATACGGATAACGATCTGAAACCAAGTATACAAATATCTCTGTTAAAGGAAG 2400
Db 2235 TTGCCACACGGCCCAACATGACACACGCTCTATACAGACTATCTGAAGTGAAGGTTTC 2294
QY 2401 CTGGGGGAATGATGTTTCGCTTTTGAATTCGGTGAAGAGCTCCGATTTGCTTAGATCA 2460
Db 2295 TTGGGGTAATGATACCTCGGGCTTAACCTTTGCTACTAGCTACCTATCCCGGTATTTAG 2354
QY 2461 AAGTCTCTATTGACAGTACATGCCCTTCATGAAATTCGCAATTTGCTATGCAATCA 2520
Db 2355 TTCTTCTATCTTTGATAGTTATGACCGTTTGCAGAAATTCAGATTTGCTATGCGACCA 2414
QY 2521 GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGAA 2580
Db 2415 AGATGACTTTAAAGAACCAACACAGAGCGCGGTCTTTGAAAGCAGCGATCTTCTCAA 2474
QY 2581 TCTTCGCTTACCTATCTCGGATCCGATTTGATAGGAATTCAGACTGCCAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACTATAGGTATTAATTTGAGAACTCTCTATGAGAGAGAGTGTCTTA 2534
QY 2641 CAATCTAACTCTTGTGTTACTGTGGATCTTGTTCGTAGTAACCCGCTGTACGACAAAC 2700
Db 2535 TGATCTTACACTGATATATACCTGTGTTGACCGTCAATATCCAAGCTGTATGACAGG 2594
QY 2701 ACTGGAATTAGCGGTGATCTTGGAACCTTCGGTAGCAATTTGGCAAGACAGCTTTT 2760
Db 2595 ATTGCGGATCAATGACGTTTCCTGGTTAACACAGCTACCAATCTTGTAGACAGCTTTT 2654
QY 2761 AGTCTCTCTGTCAGGGAACCATTTTGTCTTTAACTCAAAATTTTGAAGCCCTTTAGCAATT 2820
Db 2655 CATAGTTCCGCGGTAAACCAATTTGCTTTAACTCTGCTGGTTGAGATGTTCACTCAGT 2714
QY 2821 TTCTTTTGAATTCGCTGGTCACTCTGCAATTTACAAATTTAGAGTGTAGGAGCAAAATACCA 2880
Db 2715 TGGTTTCGAATTCAGAGCTCTTCAAGAAATTTAAGCTAGATCTTGGCGCTAAGTCCG 2774
QY 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 6

ABQ78033
ID ABQ78033 standard; DNA; 2781 BP.

XX
AC ABQ78033;

XX
DT 29-AUG-2003 (revised)

DT 03-OCT-2002 (first entry)

XX
DE Chlamydia polynucleotide SEQ ID NO 56.

XX
KW Chlamydia; antibacterial; vaccine; immune response; infection; gene; ds.

XX
OS Chlamydia caviae.

XX
FN WO200247718-A2.

XX
PD 20-JUN-2002.

XX
PP 17-DEC-2001; 2001WO-US048773.

XX
PR 15-DEC-2000; 2000US-0255839P.

XX
PA (TEXA) UNIV TEXAS SYSTEM.

XX
PI Johnston SA;

XX

DR WPI; 2002-583472/62.

XX P-PSDB; ABB98228.

PT Vaccine useful for immunizing an animal, comprising at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen.

XX Claim 6; Page 167-168; 183pp; English.

XX The invention relates to a vaccine (I) comprising at least one polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically acceptable carrier. The antigens are useful for immunising an animal, by providing at least one Chlamydia antigen or its antigenic fragment to the animal, in an amount effective to induce an immune response in the animal e.g. mammals including bovine or human. The method is effective to induce an immune response against C. psittaci, C. pneumoniae or non-Chlamydia infection. The method further involves administering to the animal an antigen or an antigenic fragment from Chlamydia species other than C. psittaci or C. pneumoniae or an antigenic fragment from a non-Chlamydia species. (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 U; 0 Other;

Query Match 18.2%; Score 546.6; DB 6; Length 2781;
Best Local Similarity 53.7%; Pred. No. 8.8e-141;
Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

QY 328 TTTTAAACACTAAGGGCGATTTCACCTTTCACAGCTAACGGGAATCTCTATTGTTCCA 387

Db 231 TTTTTCAGACTGCAGACACCTAACTTTTCAAGGGAACAACTAGCTTATCCATAAC 290

QY 388 AACCGTGTATGACGAGGCTGTAGCAGGGGCTCTGTAAACAGCAGCGGTAGATAAATC 447

Db 291 GAACCGAATGCCGAGCTAATCC---TGCAGGAATTAACGTTAACACTGCCGATAAGAT 347

QY 448 TACACGTTTATAGGGTTTTCCTCGCTATCTTTTATGCGTCTCTCGGAAGTTTCGATAAC 507

Db 348 TCTTACGCTGACAGATTTTCTTAAGTTGAGCTTTAAGGAATGCCCATCTCTCTAGTGA 407

QY 508 TACCGCAAAAGGAGCGGTAGCTCTACGCGTAGCTTGTAGTTTGACAAAAATGTCAG 567

Db 408 TACTGGAAGAGGGG---TATGAATCCGAGGAGCATTAAACTTAGCGAATAATGCCAG 464

QY 568 TTTGCTCTTCAGCAAAAATTTTCAACGGAATATGCGGTGCTATCACGCCAAAATCTCT 627

Db 465 TATTCTGTTTGAATCAGAACTATTCGCTGAGAATGGTGAGCCATCTCTTGCAGAGCTTT 524

QY 628 TTCATTACAGGAGCTACAAATGCTAGCTCTGTTTCTGAAATACCTCTCTCAAGAAAGG 687

Db 525 TTTCTTAACCGGCTCGAGCAAGAAATCAGCTTTCACCACTAATCTCTACTGCGAAAAAGG 584

QY 688 CGGAGCAATTCAGACTCCGATGCCCTTACCACTTACTGGAACCAAGGGAGTCTCTTTT 747

Db 585 TGGAGGATTTGCTGTACGGGAATAGCTCATCTTTGGGCAACCAAGGCAATCAGATT 644

QY 748 TTCTGACAAATCTCTTCGGATTCTGGAGTCAATTTTACAGAAAGCTTCGGTACTAT 807

Db 645 TTCTGGGAACACTGCTGTGAATTTCTGGGGAGCAGTATATTTCAGAAAGCTTCTATGAGAT 704

QY 808 TTCTTAATATGCTAAAGTTTCTTTTATTTGAATAAGGTCAAGAGCGAGCTCTCTCAAC 867

Db 705 TGCAGGTAAACCAACCGTTGCTTTTAGCAACAATCTGTTTCGGGTTCACTCT----- 756

QY 868 AACGGGGATATGTCAGGAGGTGCTATCTGTCTTATAAACTAGTACAGATACTAAGGT 927

Db 757 -----GATGGTTCCGGTGGAGCTATCCATTGTAGCAAAAAGGTTTCAGCCCGACCT 809

QY 928 CACCTCTACATGGAATCAGATGTTTACTCTTCAGCAACAATATCATCGAACACGCGGAGG 987

Db 810 TACTATAGAGATAACAAAGTCTTTGATTTTTCAGGGAATACTCTTCTTCAGAAAAAGGTGG 869

Db 1275 TAACCTAAAGACAAATTTACACAGCCTATCACTTTAGTGTGGTGAACCTTGTGTAAAG 1334
QY 1465 ACATGAGTGAATCTCGACAGCTCAGGCAATTCATCTCAACAGGCGAGATCTCGTCTCGAAT 1524
Db 1335 CACGGGTGTGGAAGTAGAAGCAAAACAGTCGTGCAACACAGCAGGATCTTTGATTTCTGAT 1394
QY 1525 GGACGTAGGAATCTACTCTA---GAACCTGCTGATCTAGCACCATAAACAATTTGGTTCAT 1581
Db 1395 GGATGAGGCAAAAGTTATCCGCAAAAACAGAGATGCTCACTGACGAATCTGGCTAT 1454
QY 1582 TAACATCAGTTCTATAGACGGTCAAAAGAGGCAAAAATAGAAACCAAACTACGTCAAA 1641
Db 1455 TAATCCGAATACCTTAGATGGGAAAAAATTCGCCGTAGTCGATGCCGTTCGCTGTGGAA 1514
QY 1642 AATCTGACTTTTCTGGAACCATCTTTATTTGGACCCGACGGGACGTTTATGAAA 1701
Db 1515 GAATGTGACTTTATCAGGTCTATTTGGCGTTATTTGATCCTACAGGGAAATTTTATGAAA 1574
QY 1702 TCATAGTTTAAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAGACTTCTCGAACTGT 1761
Db 1575 CCATAGCTAAATGATAGTTAGTTTAGAGGAATTCACATTTCTGGGAAAGTTCCGT 1634
QY 1762 AACAAACACCGAGTGTCTCAGATCCTAATATGAGGTGAGAAATTCATTTACGGCTATCA 1821
Db 1635 GACAAACAAACGTCCTAGTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1694
QY 1822 GGGAAAC-----TTGGGGCCCAATTTGTTGGGGACAGGGGCTTCTAGGACTGC 1869
Db 1695 AGGAAACTGT 1754
QY 1870 AACCTTCAACTGGACTAAAACTGCTATATTCCTAATCCGAGCGTATCGGCTCTTTAGT 1929
Db 1755 AATCTTTACTGGATTAATAACAGGATATGTCMAATCCTGMACTCGTCTCGCTAGT 1814
QY 1930 CCTAATAGCTTATGGAATGCAATTTATAGATATTTAGCTCTCTCAATATCTTATGGAGAC 1989
Db 1815 ACTCAATAGCTTTGGGATCCTTTATAGATTTACGTTCTTATTCAAGATGCTTTGGAACG 1874
QY 1990 TGCAAAGCAGGCTTGC---AGGAGACCGTGTCTTTTGGTGTGCTGGATATCTAATCT 2046
Db 1875 TAGTGTGTAGTATTTCTGAGACACGTCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1934
QY 2047 CTTCCATAAGATAGTACAAAAACACACGCGGGTTTCGCCATTTAGTGGCGGTATGT 2106
Db 1935 CTTCCATAAGATCGGAATCTGTAATCGAATTCGAAATCCGTCATATCAGTTCCGGATATGT 1994
QY 2107 CATAGGAGAAACCTACATATCTTGTTCAGATAAGATTTCTTAGTGTCTGCATTTTGTACGT 2166
Db 1995 GTTAGGAGCCACAAATACTCGAGAGAGGATTTCTTTAGTGTGGCTTTCTGTCAAT 2054
QY 2167 CTTTGGAGAGATAGACTACTTTTGTAGCTAAGAAATCAAGTACAGTCTACGGAGAAC 2226
Db 2055 ATTTGCAAAAGATAAAGACTACCTTTGTAAGCAAGACGCCGCAACGCTATCGGGTTC 2114
QY 2227 TCTCTATTACAGCA-----CAACGAAACCTATCTCTCTTCTTGCAGAACTACGGCC 2280
Db 2115 TGTATATTATCAGATGTGACGAGTTTGTATCTCAGCGGTTATTTAATGGGCTTAA 2174
QY 2281 TTGTGCTGTCTTATGTTCTCAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA 2340
Db 2175 CACGTGTGTTCAGGGTTTCTAAGAGATTCCTATTCTTCTTGGATGCACAAATTTACCTA 2234
QY 2341 CACCATACGATACAGTCTGAAACCAAGTATACACATATCTACTCTGTTTAAAGGAG 2400
Db 2235 TTGCCACACGGCCAAACATGACAACTCTATACAGACTATCTTGAAGTGAAGGTTTC 2294
QY 2401 CTGGGGAATGATAGTTTCTGTTTGTAGAAATTCGGTGAAGAGCTCCGATTTTGTAGATGA 2460
Db 2295 TTGGGTAATGATACCTTGGGCTTAACTTTGTCTACTAGGTACTATCCGGTATTTAG 2354
QY 2461 AAGTGTCTATTTGAGCAGTACATGCGCTTCAATGAATTTGAGTTTGTCTATGACATCA 2520
Db 2355 TTCTTCTATCTTTGATAGTATGACCGGTTTGCAAAATTAACAAGTTGTCTATGGCCACCA 2414

QY 2521 GGRAGCTTTTAAGAACACGGACACAGAGCTCGTGAATTTGGAAGTAGCCGCTCTTGTGAA 2580
Db 2415 AGATGACTTTTAAAGAACCAACACAGAGCCGGGCTTTTGAAGCAGCGATCTTCTCAA 2474
QY 2581 TCTTGTCTTACCTATCGGATCGGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACCTATAGGTATATAAATTTGAGAACTCTCTATGGAGAGAAAGTGTCTA 2534
QY 2641 CAATCTAATCTTGTGTTTACTGTGGATCTTGTTCGTAGTAACCCGACTGTAGCAAC 2700
Db 2535 TGATCTTACACTGATGTATATCTGATGTGTACCGCTCAATCCAGCTGTATGACAGG 2594
QY 2701 ACTGCGAATTTAGCGGTGATTTCTTGGAAAACTTTCGGTACGAAATTTGCAAGACAAAGCTTT 2760
Db 2595 ATTGGGATCAATGACGTTTCTCGTTTACCAGACTACGAACTTGTGTAGACAGCTTT 2654
QY 2761 AGTCTTTCGTGACGGAAACCAATTTTGTCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT 2820
Db 2655 CATAGTTTCGCGGGTAAACCATATTGCTTTAACTCTGTTGTTGAGATGTTCACTCAGT 2714
QY 2821 TCTTTTGAATTCGCTGGGTCTCTCGCAATTAACAATGTAGACTTAGGACGCAAAATACCA 2880
Db 2715 TGTCTTGAATTAAGAGCTCTTCAAGAAATTTATAAGCTAGATCTTGGCGCTAAGGTCGC 2774
QY 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 8

AAC81914
ID AAC81914 standard; DNA; 273254 BP.
XX AAC81914;
XX 15-SBP-2003 (revised)
DT 27-FEB-2001 (first entry)
XX Chlamydia pneumoniae genome DNA.
DE Genome; diagnosis; vaccine; ds.
KW Chlamydia pneumoniae.
OS Chlamydia pneumoniae.
XX WC200027994-A2.
XX 18-MAY-2000.
XX 12-NOV-1999; 99WO-US026923.
XX 12-NOV-1998; 98US-0108279P.
PR 08-APR-1999; 99US-0128606P.
XX (REGC) UNIV CALIFORNIA.

Stephens R, Mitchell W, Kalman S, Davis R;

WPI; 2000-376516/32.

Isolated nucleic acid for use in diagnostic and analytical methods
encodes genomic sequence of Chlamydia pneumoniae.

Claim 2; Page 128-320; 320pp; English.

This invention describes a novel nucleic acid (N1) encoding a Chlamydia pneumoniae protein (P1), given in the specification. The isolated nucleic acid is useful for diagnostic and analytical methods, such as, hybridization-based assays or amplification-based assays. The protein may be used for diagnostic purposes, for their enzymatic or structural activity, or as a vaccine. The invention also describes (1) a probe comprising a hybridizing fragment of N1; (2) an isolated nucleic acid (N2) that hybridizes under stringent conditions to N1; (3) an expression

CC	cassette comprising N1 under the transcriptional regulation of a
CC	transcriptional initiation region functional in an expression host, and a
CC	transcriptional termination region; (4) a cell comprising an expression
CC	cassette of (3) as part of an extrachromosomal element or integrated into
CC	the genome of a host cell as a result of induction of the expression
CC	cassette into the host cell, and the cellular progeny of the host cell;
CC	(5) a method for producing a PI comprising growing a cell of (4) where
CC	the protein is expressed and isolating the protein free of other proteins
CC	; (6) a purified polypeptide composition comprising at least 50 weight %
CC	of PI; and (7) a monoclonal antibody binding specifically to the peptide
CC	of (6). (Updated on 15-SEP-2003 to standardise OS field)
XX	
SQ	Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 U; 0 Other;
	Query Match 17.7%; Score 531.2; DB 3; Length 273254;
	Best Local Similarity 53.0%; Pred. No. 1.6e-135;
	Matches 1415; Conservative 0; Mismatches 1183; Indels 74; Gaps 10;
QY	247 TGCTGGAACTACCTACTATTAAAGGGAATGCCTCCTAGAAAATATTCCTGGAACAGG 306
DB	98349 TACTGGNATAGACTATCTCTGCAGGAGATTAATCTGTCAAAACCTTGGGATTCGG- 98407
QY	307 CACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGCGCATTTGACTTTCACAGPTAA 366
DB	98408 --CAGCTTTAACGAGGGTGTTTTTCTGCACACTACGGAATCTTTAAGCTTTCGGTAA 98465
QY	367 CGGGAACCTCTATTCTTCCAACGGTGCATCAGGACTGTAGCAGGGGTGCTGTATA 426
DB	98466 GGGGTACTCACTCTCTTTTTTAAATTAAGTCTAGTGTGAAGCGGAGACATTTCTGT 98525
QY	427 CAGCAGCGTGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATTCG 486
DB	98526 TACAACGTATAAAATCTGTCGTAAACAGATTTTCGAGTCTTACTTTCTTAGCGGCC 98585
QY	487 GTCTCTGGAGTTTGGATAACTACCGGAAAGAGCGGTAGTCTCTCTACGGGTAGCTT 546
DB	98586 ATCATCGGTAAATCACAAACCCCCTCAGAAAAGTGCAGTTAAATCTGGAGGGGATC--T 98642
QY	547 GAGTTTGCACAAAAATGTCCAGTTTGCTCTTCAGCAAAAACCTTTTCAAACGGATAATGGCGG 606
DB	98643 TACATTTGATACAATGGAACTATTTTATTAAACAAGTACTCTGAGGAATATGGCG 98702
QY	607 TGCTATCAGCGCAAAACCTCTTTTCATTAACAGGGACTCAATGTCCAGTCTGTTTTCTGA 666
DB	98703 AGGCATTTCTACCAAGAATCTTTCTTTGAAAAACAGCAGGATCGATTTCTTTTGAAGG 98762
QY	667 AAATA-----CCTCCTCAAGAAAGCGGAGCCATTACAGCTTCGGATCGCCTTAC 717
DB	98763 GAATTAATCGAGCGCAACAGGAAAGAGTGGGCTATTTGTCTACTGGTACTGTAGA 98822
QY	718 CATTTCTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTTCTGGAGC 777
DB	98823 TAATTACAATAATATACGGCTCTTACCCTCTTCTCGAACAAATATGCTGAAGCTGCAGGTGG 98882
QY	778 TGCAAATTTTACAGAAGCTCGGTGACTATTTCTAAATATGCTAAAGTTTCTTTTATTTGA 837
DB	98883 AGCTATAAATAGCACAGGAAACCTGTACAATTAACAGGAATACGCTCTCTGTATTTCTTGA 98942
QY	838 CAATAAGGTCACAGGAGCGAGTCTCTTCAACAAACGGGGATATGTCCAGGAGGTGCTATCTG 897
DB	98943 AAATAGTGTGAC---AGCGACCCAGGAATGGAGGAGCTCTTTCTGGAGATGCG--- 98995
QY	898 TGCATTATAAAGTGTACAGATCTAAGTGTCAACCTCACTGGAATACAGATGTTACTCTTT 957
DB	98996 -----ATGTTTACCATACTCTGGAATCAGAGTGTAACTTTT 99029
QY	958 CAGCAACAATATACGACAAACAGCGGGAGAGCTATCTATGTGAAAAAGCTCGAACTGGC 1017
DB	99030 CTCAAGNAACCAAGCTGTAGCTTAATCGCGAGAGCAATTAATGCTAAGAACTTCACTGGC 99089
QY	1018 TTCGGAGGACT-----TACCTTATTCATAGAAATAGTGTCAATPGGAGGTACAGTCTCT 1072
DB	99090 TTCGGGGGGGGGGGTATCTCTTTTCTCAACAATATAGTCCAAAGTACCACTGCAGGT 99149

Qy	607	TGCTATCACCGCAAAACTCTTTTCATTAACAGGGACTACAAATGTCAGCTCTGTGTTTCTCGA	666
Db	510	AGCCATTTTACCAAGAATCTTTCTTTTGA AAAACAGCACGGATCGAATTTCTTTTGAAGG	569
Qy	667	AAATA-----CCTCTCAAGAAGCGGAGCCATTACAGACTTCCGATGCCCTTAC	717
Db	570	GAATAAATCGAGCGCAACAGGGA AAAAGGTGGGGCTATTGTGCTACTGGTACTGTAGA	629
Qy	718	CATTACTGGAAACCAAGGGGAAGTCTCTTTTTCGACAATACTTCTTCGGAATCTCGAGC	777
Db	630	TATTACAAATTAATACGGCTCCTACCCCTCTCTCGAA CAATATTCTCGAAGCTCGAGTGG	689
Qy	778	TGCAATTTTACAGAGCCTCGGTGACTATTTCTTAATAATGCTAAAGTTTCCTTTATTGA	837
Db	690	AGCTATAAATAGCACAGAAACTGTACAAATTACAGGGAATACGTCCTCTGTATTTTTCTGA	749
Qy	838	CAATAAGGTACAGAGCGAGCTCCTCAACAA CGGGGATATGTCAGAGAGTGTCTATCTG	897
Db	750	AAATAGTGTGAC---AGCGACCGCAGGAATGAGGAGCTCTTTCTCGAATGCCG----	802
Qy	898	TGCTTATAAAACTAGTACATATAAGGTCACCTCACTGGAATCAGAGTTTACTCTTT	957
Db	803	-----ATGTTACCATCTGGGATCAGAGTGTACTTT	836
Qy	958	CAGCAACAATACATCGACAACAGCGGAGAGCTATCTATGTGAAAAGCTCGAAGTGGC	1017
Db	837	CTCAGAAACCAAGCTGTAGCTAATGCGGAGCCATTTATGCTAAGAAGCTTACACTGGC	896
Qy	1018	TTCCGGAGGACT-----TACCCTATTCACTAGAAATAGTGTCAATGGAGGTACAGTCC	1071
Db	897	TTCCGGGGGGGGGGGTATCTCCTTTTCTTAACAA TATAGTCCAAAGTACCAGTGCAGG	956
Qy	1072	TAAAGGTGGGCCATAGCTATCGAAGATAGTGGGGAATTCAGTTTATCCCGCGATAGTG	1131
Db	957	TAATGTTGGAGCAATTTCTATATCTGGCAGCTGGAGAGTGTAGTCTTTCAGCAGAGCAGG	1016
Qy	1132	TGACATGTTCTTTTTAGGGAATA CAGTCACTTCCTACTCTCC---TGGGACGAATAGAAG	1188
Db	1017	GGACATTTACCTTCAATGGGAATGCCATGTTGTCAA CTACACCAAAACTACAAAAAGAAA	1076
Qy	1189	TAGTATCGACTTAGGAACGAGTGC AAGATGACAGCTTTGGGTTCTGCTCTCGTAGAGC	1248
Db	1077	TTCTATTGACATAGGATCTACTCGAAAGATCA GGAATTTACGTGCAATATCTCGGCATAG	1136
Qy	1249	CATCTACTCTTATGATCCCACTACTCAGGATCATCCACAACAGTTTACAGATGCTTTAAA	1308
Db	1137	CATCTTTTCTACGATCCGATTA CTGCTAATACGGCTGCGGATTTACAGATACTTTAAA	1196
Qy	1309	AGTTAATGAGACTCCGGCAGATTCTGCATCAATATACAGGGAACATCATCTTCACAGG	1368
Db	1197	TCTCAATAAGCTGATGCAGTAAATAGTACAGATTATAGTGGGTGCGATTGTTTTTCTGG	1256
Qy	1369	AGAAAGTTATCAGACACAGGCGCGAGATTCTA AAAATCTTACTTCGAAAGTACTACA	1428
Db	1257	TGAAAGCTCTCTGAAGATGAAGCAAAGTTG CAGACAACCTCACTTCTACGCTGAAGCA	1316
Qy	1429	GCCTGTAACTCTTTTCAGAGGTACTTATCTTTAAAACATGGAGTGAAGTCTCTGCAGACTCA	1488
Db	1317	GCCTGTAACTCTTAATCGAGAAATTTAGTACTTTAAACGTGGTGTCACTCTCGATAGAA	1376
Qy	1489	GGCATTCACTCAACAGCGCA GATTCTCGTCTCGAAATGGACGTAGGAACTACTCTGAAGACC	1548
Db	1377	AGGCTTTACTCAGACCCGGGTTCTCTGTATTATGTGATCGGGCACAACGTTAAAAGC	1436
Qy	1549	---TGCTGATCTAGCACCATTAACATTTGGTCAATTAACATCAGTTCTATAGACGGTGC	1605
Db	1437	AAGTACAGAGGAGGTCACTTTAACAGGTCTTTCCATTTCTGTAGACTCTTTTAGCGAGGG	1496
Qy	1606	AAAGAAAGCAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTTACTCGAACCAT	1665
Db	1497	TAGAAAGTTGTAATTCGTCTGCTCTCGCAGCAAGTAAAAATGTAGCCTTAGTGTCCGAT	1556
Qy	1666	CACTTTATGGACCCGACGGGCACGTTTTATGAAATATAGTTTAAAGAAATCCTCAGTCT	1725

Db	1557	TCCTCTTTTGGATTAACCAAGGGAATGCTTAATGAATAATCACGACTTAGGAAAAAACTCAAGA	1616
Qy	1726	CTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAAACAAGCACCGCAGTGACTCCAGA	1785
Db	1617	CTTTTCATTTGTGCAGCTCTCTGCTGGGTCTGTCAACAACATACAGATGTTCCAGCGGT	1676
Qy	1786	TCCTTAATCGGTGAGAAATCCATTAAGCGCTATCAGGGAACCTTGGGGCCCAATTTGTTG	1845
Db	1677	TCCTACAGTAGCAACTCTCAGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGT	1736
Qy	1846	GG-----GGACAGGGGCTTCTACGACTGCAACTTCAACTGGACTAAAACTGG	1893
Db	1737	TGATGATACCGCAAGCACTCCAAGACTAAGACAGCGACATTAGCTTTGNAACCAATACAGG	1796
Qy	1894	CTATATTCTTAATCCCGAGGGTATCGGCTCTTTTAGTCCCTTAATPAGCTTATPGGAATGCAATT	1953
Db	1797	CTACCTTTCCGAATCCTGAGCGTCAAGGACCTTTAGTTTCTTAATPAGCTTTGGGGATCTTT	1856
Qy	1954	TATAGATATTAGCTCTCTCCATTATCTTATGGAGACTGC AAAAGAAAGGGTTGCAGGAGA	2013
Db	1857	TTCAGACATCCAGCGATTCAGGTTCTATAGAGAGAGTGCTTTGACTTTTGTGTTCA	1916
Qy	2014	CCGTCCTTTTGGTGTCTGGATTATCTAACTTCTTCCATPAGGATAGTACAAAAACAG	2073
Db	1917	TCGAGGCTTCTGGCTGCGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAA	1976
Qy	2074	ACGGGGTTTCGCCATTTAGTTCGGGTTATGTCATAGGAGGAAACCTACATACTTTGTTTC	2133
Db	1977	ACGCAAAATCCGTCAATAAATCTCGTGATATGCTATCGAGGTGCAGCGCAACTTTGTTTC	2036
Qy	2134	AGATAAGATTCTTAGTGTCTGATTTTGTACGCTCTTTTGGAAAGATAGAGACTACTTTGTT	2193
Db	2037	TGAAAACCTTAATTAGCTTTTGCCACTCTTTTGGTAGCGATAAGATTTCTTAGT	2096
Qy	2194	AGCTAAGATTCAGGTACAGTCTACGAGGAACTCTCTATTAACAGACAAAGAAACCTTA	2253
Db	2097	CGCTAAAAATCACTGATACCTATACGAGGCTTCTATATCCAAACATTAACAGAAATG	2156
Qy	2254	TATCTCTCTCTCTGCAAACTACGGCTTGTTCGTTGTCTTATGTTCTTACAGAGATTC	2313
Db	2157	TAGTGGGTTCAATAGTTGTCTTTAGATAAA-----CTTCTTGCTCTTGGAGTCATAAAC	2213
Qy	2314	TGTTCTCTTTTCAGGAAACCTTAGTACACCCATACGGATAACGATCTGAAAAACCAAGTA	2373
Db	2214	CCTCGTTTTAGAAGGCGAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTA	2273
Qy	2374	TACAACATATCTTACTGTTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAAATCCG	2433
Db	2274	TACTGGGATATCTCGAGGTGAAGGTTCTTGGGGGAATAATGCTTTTAAATGATGTTGGG	2333
Qy	2434	TGGAAGAGCTCCGATTTGCTTAGATAAAGATGCTCTATTGTAGCAGTACATGCCCTTCAT	2493
Db	2334	AGCTTCTTCTCATCTTATCTCGTAATACCTGCAATGTTTTGATACCTATGCTCCATACAT	2393
Qy	2494	GAAATTCAGTTGTCTATGCAATCAGGAAGGTTTTAAAGAACAGGGAACAGAGCTCG	2553
Db	2394	CAAACTGAATCTGACCTATATAGCTCAGGACAGCTTCTCGGAGAAAGGTACAGAGGAAG	2453
Qy	2554	TGAATTTGGAAGTAGCGGCTCTGTGAAATCTTGCTTTACCTATCGGGATCCGATTTGATAA	2613
Db	2454	ATCTTTTGATGACAGCAACCTCTTCAATTAATCTTTGCCCTATAGGGTGAAGTTGAGNA	2513
Qy	2614	GGAACTCAGACTGCCAGATGCAACGTACAACTTAATCTTTGTTTATCTGTGCACTTTGT	2673
Db	2514	GTCTCTGATTTGAATGACTTTTCTTATGATCTGACTTTATCCTATGTTTCTCTGATCTTAT	2573
Qy	2674	TCGTAGTAAACCCGACTGTACGACACACTGCGAATTAGCGGTGATTTCTTTGGAACCTTT	2733
Db	2574	CCGCAATGATCCCAATGCACTACAGCATTTGTAATCAGCGGAGCCTCTTGGGAAACTTA	2633
Qy	2734	CGGTACGAATTTGGCAAGACAAGCTTTAGTCTCTCTGTCAGGGAACCAATTTTGTCTTAA	2793

Db 2634 TGCCAATAACTAGACACGACGAGCCCTTGCAAGTGGTGCAGGAGTCACTACGCGCTTCTC 2693
 Qy 2794 CTCAATTTTGAAGCTTTAGCCAAATTTCTTTTGAATTCGGTGGTCACTCGCAATTA 2853
 Db 2694 TCCTATGTTTGAAGTGTCTCGGCCAGTTTGTCTTTGAAGTTCTGTGGATCCTCACGGATTA 2753
 Qy 2854 CAATGTAGCTTAGGAGCAAAATACCAATCTTA 2886
 Db 2754 TAATGTAGATCTTGGGGGTAAGTCCAAATCTTA 2786
 RESULT 10
 ABL91231
 ID ABL91231 standard; DNA; 2787 BP.
 XX
 AC ABL91231;
 XX
 DT 29-AUG-2003 (revised)
 DT 29-JUL-2002 (first entry)
 XX
 XX Chlamydia pneumoniae cp0010 ORF DNA, SEQ ID NO:96.
 DE
 XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029; open reading frame; ORF; gene; ds.
 XX
 OS Chlamydothila pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2787
 FT /*tag= a
 FT /product= "cp0010"
 FT sig_peptide 1..75
 FT /*tag= b
 FT mat_peptide 76..2784
 FT /*tag= c
 FT /product= "Mature protein"
 XX
 XX W020202606-A2.
 FN
 XX 10-JAN-2002.
 PD
 XX 03-JUL-2001; 2001WO-IB001445.
 XX
 XX 03-JUL-2000; 2000GB-00016363.
 PR 11-JUL-2000; 2000GB-00017047.
 PR 21-JUL-2000; 2000GB-00017983.
 PR 07-AUG-2000; 2000GB-00019368.
 PR 18-AUG-2000; 2000GB-00020440.
 PR 14-SEP-2000; 2000GB-00022583.
 PR 10-NOV-2000; 2000GB-00027549.
 PR 22-DEC-2000; 2000GB-00031706.
 XX
 XX (CHIR-) CHIRON SPA.
 XX
 XX Ratti G, Grandi G;
 XX
 XX WPT; 2002-154726/20.
 DR N-PSDB; ABB90573.
 XX
 XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
 FT
 XX Claim 5; Page 88-89; 364pp; English.
 PS
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is

CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 2787 BP; 785 A; 568 C; 619 G; 815 T; 0 U; 0 Other;
 Query Match 17.6%; Score 527; DB 6; Length 2787;
 Best Local Similarity 52.9%; Pred. No. 2.5e-135;
 Matches 1413; Conservative 0; Mismatches 1185; Indels 75; Gaps 10;
 Qy 247 TGCTGGAACCTACCTACCTATTTAAGGGAAATGTCACCTAGAAAATATTCCTGSAACAGG 306
 Db 156 TACTGGAAATAGACTATCTCTGACAGAGATATACTCTGCAAAACCTTGGGATTCCG- 214
 Qy 307 CACAGCAATCACAAAAGCTGTTTAAACAACACTAAGGGCGATTGACTTTTCACAGTAA 366
 Db 215 --CAGCTTTAAACGAAGGTTGTTTTCTGACACTACGGAATCTTTAAGCTTTGCCGTAA 272
 Qy 367 CGGGAACCTCTATTGTTCCAAACGGTGGATGACGAGCACTGTACGAGGGGCTGCTGTTAA 426
 Db 273 GGGGTACTCACTTTCTTTTTTAAATATTAAGTCTAGTCTGAAGGCGCAGCACTTCTGT 332
 Qy 427 CACGAGCGTGTAGATAAATCTACCGTTTATAGGGTTTCTTCGCTATCTTTTATTGC 486
 Db 333 TACAACCTGATAAAATCTGCTGCTAACAGGATTTTCAGTCTACTTTCTAGGCGGCC 392
 Qy 487 GTCTCTCTGGAAGTTTCGATAACTACCGCAAGAGCGCTGTAGTCTCTACGGGTAGCTT 546
 Db 393 ATCATCGGTAATCACAAACCCCTCAGGAAAGGTGCAGTTAAATGTGGAGGATC--T 449
 Qy 547 GAGTTTGACAAAATGTGAGTTGCTCTTCAGCAAAAACCTTTTCAACGGAATATGSCGG 606
 Db 450 TACATTTGATAACAATGGAACTATTTTATTAACAAGATTTACTGTGAGGAAATGSCGG 509
 Qy 607 TGCTATCACCGCAAAAACCTCTTTCAITTAACAGGAGCTACAAATGTCAGTCTGTGTTTCTGA 666
 Db 510 AGCAATTTCTACCAAGNAATCTTTCTTTGAAAACACAGCACGGATCGATTTCTTTGAAG 569
 Qy 667 AAATA-----CCTCCTCAAAGAAAGCGGAGCCATTCAGACTTCCGATGCCCTTAC 717
 Db 570 GAATAAATCGAGCGCAACAGGGAAAAAGGTGGGGCTATTTGTGCTACTGGTACTGTAGA 629
 Qy 718 CATTACTGGAAACCAAGGGGAAGTCTCTTTTCTGCAAACTACTTCTTCGGATTCGAGC 777
 Db 630 TATTACAAATAATACGGCTCTCTACCCCTCTTCTCGAACAATATTGCTGAAGCTGCAGTGG 689
 Qy 778 TGCAATTTTACAGAGCCTCGGTGACTATTTCTAATAATGCTAAAGCTTTCTTTTATTGA 837
 Db 690 AGCTATAAATAGCACAGGAAACTGTACAATTACAGGAATACGCTCTCTGTATTTCTGA 749
 Qy 838 CAATAAGGTCACAGGAGCGAGCTCCTCAACAACCGGGGATATGTTCAGAGAGTGTCTATCTG 897
 Db 750 AAATAGTGTGAC---AGCGACCGCAGGAAATGGAGGAGCTCTTTCTGGAGATGCCG--- 802
 Qy 898 TGCTTATAAACTAGTATACAGATACTAGGTCACCTCCTCAGTGAATCAGATGTACTCTT 957
 Db 803 -----ATGTTACCATACTCTGGAAATCAGAGTGTAACTTT 836
 Qy 958 CAGCAACAATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGCTGGC 1017
 Db 837 CTGAGGAACCAAGCTGTAGCTTAATGCGGAGCGCAATTTATGCTTAAGAACTTACACTGGC 896
 Qy 1018 TTCGGGAGGAC-----TTACCCCTATTTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCC 1071

Db 897 TTCCGGGGGGGGGGGTATCTCTCTTTTAAACAATAATAGTCCAAAGGTACCACTGCAGG 956
Qy 1072 TAAAGGTGAGCCATAGCTATCGAAGATAGTGGGAAATTGAGTTTATCGCGCGATAGTGG 1131
Db 957 TAAAGGTGAGCCATTTCTATCTGCGAGCTGGAGAGTGTAGTCTTTTACAGCAGAACGCG 1016
Qy 1132 TGACATATGCTTTTATAGGAATACAGTCACTTCTACTACTCC---TGGGACGAATAGAAG 1188
Db 1017 GGACATATACCTTCAATGGGAATGCCATTTGTCACTACACCAAACTACAAAAGAAA 1076
Qy 1189 TAGTATCGACTTAGGAACAGAGTGAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGC 1248
Db 1077 TTCTATGACATAGGATCTACTGCAAAAGATCAGAAATTTACGTGCAATATCTGGGCATAG 1136
Qy 1249 CATCTACTTCTATGATCCCAATAACTACAGGATCATCCAAACAGATTACAGATGTCTTAAA 1308
Db 1137 CATCTTTTCTACGATCCGATTACTGCTAATACGGCTGCGGATTCTACAGATCTTTAAA 1196
Qy 1309 AGTTAATGAGCTCCGGGAGATTTCTGCACTACAAATACAGGAACATCATCTTCACAGG 1368
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Qy 1369 AGAAAGTTATCAGACACAGAGCCGACAGATTCTAAATAATCTTACTTTCGAAGCTACTACA 1428
Db 1257 TGAAGAAGCTCTGGAAGTGAAGCAAAAGTTGACAGACACCTCACTTCTACGCTGAAGCA 1316
Qy 1429 GCGTGAATCTTTTACGAGGTACTCTATCTTTTAAACATGAGTACGACTCTGACAGACTCA 1488
Db 1317 GCGTGAATCTTAACTGACAGGAATTTAGTACTTAAACGTGGTGTCACTCTCGATACGAA 1376
Qy 1489 GGCATTCATCAACAGGAGATTTCTGCTCGAAATGGAGCTAGGAACCTACTCTAGAAC 1548
Db 1377 AGCGTTTACTCAGACCGCGGTCTCTGTTATATGAGTGGGCGACACGTTAAAGC 1436
Qy 1549 ---TGCTGATACTAGCACCATAAACAATTTGGTCAATTAACATCAGTTCTATAGACGGTGC 1605
Db 1437 AAGTACAGAGGAGTCACTTTAAACAGTCTTTCCATTCTGTAGACTCTTTAGGCGAGG 1496
Qy 1606 AAGAAGGCAAAATAGAAACCAAGCTACGTCAAAATAATCTGATTTTATCTGGAACCAT 1665
Db 1497 TAAGAAAGTTGAATGTCTCTGCGCAAGTAAATAATGAGCCCTTAGTGTCCGAT 1556
Qy 1666 CACTTTATTTGGACCGGACGCGGCTTTTATGAATCATAGTTTAAAGAAATCTCAGTC 1725
Db 1557 TCTTCTTTTGGATAACCAAGGGAATGCTTATGAATAATCAGCTTAGGAAATACTCAAGA 1616
Qy 1726 CTACGACATCTTAGAGCTCAAAAGCTTCTGGAACGTGAACAAGCACGCGAGTCACTCCAGA 1785
Db 1617 CTTTTCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACAACTACAGATGTTCCAGCGT 1676
Qy 1786 TCTATAATGGGTGAGAAATTCATTTACGGCTATACAGGAACCTTGGGCGCCAAATTTGTTG 1845
Db 1677 TCTACAGTAGCAACTCTCTACGCACTATGCGGTATCAAGGTACTTGGGGAATGACTTGGGT 1736
Qy 1846 GG-----GGACAGGGGCTTCTACGCTGCAACCTTCACTGGACATAAACTCG 1893
Db 1737 TGATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACATAGCTTGGACCAATACAGG 1796
Qy 1894 CTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTT 1953
Db 1797 CTACCTCCGMAATCTGAGCGTCAAGACCTTTAGTTCCTAATAGCTTTGGGATCTTT 1856
Qy 1954 TATAGATATAGCTCTCTCCATTAATTTATGAGACTGCAACGAAGGGTTGAGGGAGA 2013
Db 1857 TTCAAGACATCCAAAGCGAATCAAGGTGTCTATAGAGAAAGTGTCTTTCACCTCTTTGTTTCA 1916
Qy 2014 CCGTGTCTTTTGGTGTGGATATCTAATCTTCTTCCATAGGATAGTACAAAAACAG 2073
Db 1917 TCGAGGCTTCTGGGCTGCGGAGTCCGCAATTTCTTAGATAAGATAAGAAAGGGGAAA 1976
Qy 2074 ACGCGGTTTTCGCCATTTTGGTGGCGGTTATGTCATAGGAGGAAACCTACATCTTTGTTTC 2133
Db 1977 ACGCAATACCGTCAATAATCTGGTGATATGCTATCGGAGGTGCGCGCAACTTTGTTTC 2036

Qy 2134 AGATAAGATCTTAGTGTGCTGCAATTTTGTGTCAGTCTTTTGGAAAGATAGAGACTACTTTGT 2193
Db 2037 TGAATACTTAATAGCTTTGCTTTGCCAACTCTTTGGTAGCGATAAAGATTTCTTAGT 2096
Qy 2194 AGCTAAGATCAAGGTACAGTCTACGGAGGAATCTCTATTACCAGCAACAGAAACCTA 2253
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Db 2157 TAGTGGGTTCAATAGTTGTCTCTTAGATAAA---CTTCTGCTCTTGGAGTCATAAAC 2213
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Qy 2434 TGAAGAGCTCCGATTTGCTTAGATGAAGTGTCTATTTGAGCAGTACATGCCCCTTCA 2493
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Qy 2494 GAAATTCAGTGTGCTATGCAATCAGGAAGGTTTAAAGAACAGGGAACAGAGCTCG 2553
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Qy 2554 TGAATTTGGAAGTAGCCGCTTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAA 2613
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Db 2634 TGCCATAATCTTAGCAGCAGCGCTTGAAGTGTGCGAGCAGTCACTACGCTTCTC 2693
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RESULT 11

AAZ61509
ID AAZ61509 standard; DNA; 2957 BP.
XX
AC AAZ61509;
XX
DT 15-SEP-2003 (revised)
DT 19-JUN-2000 (first entry)
XX
XX DNA encoding the CPN100395 polypeptide.
XX CPN100395; Chlamydia infection; immune response; vaccine; ss.
XX Chlamydia pneumoniae.

Key Location/Qualifiers
FH 101..2857
FT CDS /*tag= a
XX

PN WO200011193-A2.
XX 02-MAR-2000.
XX 18-AUG-1999; 99WO-IB001449.
XX 20-AUG-1998; 98US-0097187P.
XX 20-AUG-1998; 98US-0097188P.
XX 20-AUG-1998; 98US-0097189P.
XX 20-AUG-1998; 98US-0097190P.
XX 20-AUG-1998; 98US-0097195P.
XX 20-AUG-1998; 98US-0097196P.
XX 20-AUG-1998; 98US-0097197P.
XX 27-AUG-1998; 98US-0097191P.
XX 17-AUG-1999; 99US-00376770.
XX (CONN-) CONNAUGHT LAB LTD.
XX Murdin AD, Oomen RP;
XX WPI; 2000-224703/19.
XX P-PSDB; AAY69369.
XX Novel antigens and corresponding DNA molecules that can be used to
XX prevent, treat and diagnose disease caused by Chlamydia infection in
XX mammals, especially humans.
XX Claim 1; Fig 15-E; 201pp; English.
XX AAZ61502-09 encode Chlamydia pneumoniae polypeptides. The polypeptides
XX are present in the bacterial membrane structure, in the external vicinity
XX of the membrane structure, in the inclusion membrane structure, in the
XX external vicinity of the inclusion membrane structure, and in the
XX cytoplasm of the infected cell. The polypeptides may be used to prevent,
XX treat and detect the presence of Chlamydia infection and/or the presence
XX of Chlamydia in a sample. The polypeptides may also be used to induce an
XX immune response in a mammal. The vaccine vector comprising the
XX polynucleotides is used to induce an immune response in a mammal.
XX Antibodies directed against the polypeptides may also be used
XX therapeutically to treat and/or prevent a Chlamydia infection. (Updated
XX on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 2957 BP; 818 A; 598 C; 683 G; 858 T; 0 U; 0 Other;
XX
XX Query Match 17.5%; Score 524.6; DB 3; Length 2957;
XX Best Local Similarity 53.4%; Pred. No. 1.2e-134;
XX Matches 1424; Conservative 0; Mismatches 1159; Indels 84; Gaps 12;
XX
QY 242 GAAGATGCTGGAACTACCTACCTATTTAAGGGAATGTCTCTAGAAAATATTCCTGGA 301
DB 260 GATGCTAGTGGCAGACCTATATTCTCGATGGGATGTCTCGATA--AGCCAAAGCAGGG 316
QY 302 ACAGGCACAGCAATCACAAAAGCTGTTTAAACAACACTAAGGCGATTTGACTTTCACA 361
DB 317 AAACAAACGAGCTTAACCAAGTGTGTTTCTTAAACACTGACAGGAATCTTACCTTCTTA 376
QY 362 GGTAAACGGAATCTCTATTTGTTCCAAACGGTGGATGACGGGACTGTAGCAGGGGTGCT 421
DB 377 GGGAAACGGAATTTCTCTTCAATTTTGAACATATATTTTGGTCTACTGTGTCAGGTGTGTT 436
QY 422 GTTAAACAGAGCGTGGTAGATAAATCTACACGTTTATAGGGTTTCTTTCGCTATCTTTT 481
DB 437 GTTAGCAATACAGCAGCTTCTGGGATTTACGAAATTTCTCAGGATTTTCAACTCTTCGATG 496
QY 482 ATTGCGTCTCTCGAAGTTCGATAAATCTACCGCAAGGAGCCGTTAGTCTCTACGGGT 541
DB 497 CTTGCAAGTCTCT-----AGGACACAGGTAAAGGAGCCATTAATAATTCACCGATGT 547
QY 542 AGCTTGAGTTTGCACAAAATGTCAAGTTTCTTTCAGCAAAAATTTTCAACGGGATAAT 601
DB 548 --CTGGTGTGAGATAGGGAATCTTGATCTT-AAAGAAATGCCTTAGTGAAT 604
QY 602 GCGGTGCTATACCCGCAAAAATCTTTTCAATTAACAGGAGCTACAATGTCTGCTCTGTTT 661

DB 605 GGGGAGCCATCAATACAGAGACTTTGTCTTTGACTGGGAGTACGCGTTTTGTACGCTTC 664
QY 662 TCTGAAAATACCTCTCAAGAAAAGGGAGCCATTTCAGACTTCGATGCGCTTACCATT 721
DB 665 CTTGGCAATAGCTCGTCAACAAGGGAGCGATCTATGCTTCTGGTGACTCTGTGAT 724
QY 722 ACTGGAACCAAGGGAGTCTCTTTTCTGACAATCTTCTTCCGATCTTGGAGTCTGAGCTGCA 781
DB 725 TCTGAGAAATGCAGGAATCTTTGAGCTTCGGAACAACACAGTGCACAATCAGGAGCGCG 784
QY 782 ATTTTACAGAAGCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTTTTATTGACAA 841
DB 785 ATCTCTGCTGAAGGAACCTTGTGATCTCCAAATCAAAATATCTTTTTCGATGGCTGC 844
QY 842 AAGTCAAGGAGCGAGCTCTCAACAACGGGGATATGTCAAGAGGTGCTATCTGTCT 901
DB 845 AAAGCAACTACAATGGCGAGCTATTGATTGTAACAAGCAGGG----- 890
QY 902 TATAAAACTAGTACAGATACCTAGTCACTCTGGAATCAGATGTACTCTTCAAGC 961
DB 891 -----CGAACCCAGACCTCTCTTCTGACTCTTTTCAGGAATGAGAGCTGCAATTTCTG 943
QY 962 AACAAATACATCGACAACAGCGGAGGAGCTATCTATCTGAAAAAGCTCGAACTGCTTCC 1021
DB 944 AATAACACAGCAGGAATAGTGGAGTGCATTTATACCAAAAATTTGGTGTGTTATCTCTCA 1003
QY 1022 GGAGGACTTACCCTATTTCAGTAGAATAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGGA 1081
DB 1004 GGACGAGGAGGAGTGTATTCTTCTAAACAAGCTGCGAATGCTACTCTCTAAAGGAGGG 1063
QY 1082 GCCATAGCTATCAAGATAGTGGGAAATTCAGTTTATCCCGCATAGTGTGTGCAATTGTC 1141
DB 1064 GCAATTGCGATCTAGATCTCGAGAGATTAGCAATTTCTCAGATCTCGGCAATATCAT 1123
QY 1142 TTTTATAGGAAATACAGTCACTTCTAC-----TACTCTCGGAGGATAGAGTATGATTC 1195
DB 1124 TTGAGGCGCAATACTAGGACATCTACAGGAGTCTCGGAGTGTGACCAAAATGCTATA 1183
QY 1196 GACTTAGAACGAGTGCAGAGTGAAGATGACAGCTTTTCGTTCTGCTGTGTAGAGCCATCTAC 1255
DB 1184 GATCTTGATCGAATGCMAAATTTTAAATCTCCGAGCGACTCGGGGAAATAAGTTATT 1243
QY 1256 TTCTATGATCCCAATAACTACAGGATCATCCACAACAGTTTACAGATGCTTTAAAGTTAAT 1315
DB 1244 TTATATGATCTTATCAGG-----GCTCAGGAGCTACTGATAAGCTCTCTTTTGAAT 1294
QY 1316 GAGACTCCGCGAGATCTGCACTACATAATACAGGGAACATCATCTTTCACAGAGAGAAAG 1375
DB 1295 AAAGCTGACGAGGATCTGGAATACCTATGAAGGCTACATCGTTTCTCTGAGAGAGAA 1354
QY 1376 TTATCAGACAGAGCGCGAGATCTTAAATAATCTTTCGAAAGCTACTTACAGCCCTGTA 1435
DB 1355 CTCTCAGAAAGAGAACTTAAGAAACCTGACAATCTGAAGTCTACATTTACACAGGCTGTA 1414
QY 1436 ACTCTTTTCAGGAGTACTCTATCTTTTAAACATGGAGTGACTCTGCAGACTCAGGCAATTC 1495
DB 1415 GAGCTTGTCTGAGGTGCTTTAGTTTGAAGATGGAGTGAAGTGTAGTTCGAAATACTATA 1474
QY 1496 ACTCAACAGCGAGATCTCGTCTCGAAATGGAGGAGTGAAGTGAAGTCTAGTCTAGTCT 1552
DB 1475 ACGAGGTGAGGAGTGAAGTCTGTTATGATGGAGGAGTACTCTTTGAGGCAAGCTT 1534
QY 1553 GATCTAGCAGCAATAAATAATTTGGTCAATTAACATCAGTCTTATAGACGGTGCAGAAAG 1612
DB 1535 GAGGGGTCACTCTCAATGGCCCTAGCCATTAATATAGATTCCTTTAGATGGGCAATAATA 1594
QY 1613 GCAGAAATAGAACCAAGCTAGTCAAAAATCTGACTTTTATCTGGAACCATCACTTTA 1672
DB 1595 GTATCATTAAGCGCAGCGCAAGTAAAGGATGTTCCTTATCAGGGGCTCATGCTT 1654
QY 1673 TTGGAGCCCGGAGCGGCTTTTATGAAATCATAGTTTAAAGAAATCTCAGTCTCAGGAC 1732

Db 1655 GTAGATGCTCAGGGAACTATTATGAGCATCATAACTCAGTCAACAGCAGGCTCTTTCCT 1714
Qy 1733 ATCTTAGAGCTCAAGACTTCTGGAACTCTACAGACCGCAGTACCTCCAGATCCTATA 1792
Db 1715 TTAATAGAGCTTCTGCAAGAGAACGATGACTACTACAGATATCCCCGATACCCCAATT 1774
Qy 1793 ATGGGTGAGAAATTCATTTAGCGCTATCAGGAACTTGG-----GGCCCAATTGTTTGG 1846
Db 1775 CTAATACTAGATCATTGCTATGGGTATCAAGGAACTGGAATATTTGTTGGTGCAGCAT 1834
Qy 1847 GGGCAGGGGCTTTACAGCTCAACCTTCAACTGGATAAATCGGCTATATCTCTAAT 1906
Db 1835 GCAACTGCAAAAACAAAAATGCTACCTTAACCTTGAACCTAAACAGGATACAAGCCGAAT 1894
Qy 1907 CCCAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGC 1966
Db 1895 CCAGAACGTAGGGACCTTGGTCTCTAATAGCCTGTGGGGTCTTTTGTGATGATCGCG 1954
Qy 1967 TCTCTCCATTATCTTATGAGACTGCAACGAAGGGTTGCGAGGAGCCGTGCTTTTGG 2026
Db 1955 TCCATTGAGAGCTCATGACCGGAGCACAACTTCTGTTATCTTCGCAACAAATTTGGT 2014
Qy 2027 TGTGTGGAATATCTAACTTCTTCATAGGATAGTACAAACAGAGCGGGTTTGGC 2086
Db 2015 GTATCAGGAATCGCGACTTTTGTGATGAAGATCAGAAAGGAAACCAAGCTAGTTATCGT 2074
Qy 2087 CATTTGAGTGGCGTTATGTCATAGGAGAAACCTACATACCTTGTTCAGATAAGATCTT 2146
Db 2075 CATTTAGCGGGTTATGCATTAGGAGGAGATCTTCACGGCTTCTGAAAATTTCTTT 2134
Qy 2147 AGTGTGCTATTTTGTGAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAACTAA 2206
Db 2135 AATTTTGTCTTTTGTGAGCTTTTGGCTAGCAAGGACCATCTTGTGGCTAAGAACCAT 2194
Qy 2207 GGTACAGTCTAGGAGGAATCTCTATATACAGCAACAACTATATCTCTCTCT 2266
Db 2195 ACCCATGTATATGCGGGGCAATGAGTTACCGACACCTCGGAGAGTCTAAGACCCCTCGT 2254
Qy 2267 TGCMAACTAGCGCTTTGTTGTTCTTATGTTCTTACAGAGATTCCTGTCTCTTTTCA 2326
Db 2255 AGAT-----TTTGTGAGAAATCTGACTCCCTACCTTTTGTCTCAAT 2299
Qy 2327 GGAACCTTAGCTACACCCATACGATACGATCTGAAAACCAAGTATACAACTATCT 2386
Db 2300 GCTCGGTTTGTCTATGACCATACCGACATAACATGACCAAAAGTACACTGGCTATTCT 2359
Qy 2387 ACTGTTAAAGAGCTGCGGGAATGATAGTTTGGCTTTAGAAATTCGGTGAAGAGCTCG 2446
Db 2360 CCTGTTAAGGGAAGCTGGGGAAATGATGCTTCGGTATAGATGTGGAGAGCTATCCCG 2419
Qy 2447 A---TTTGTCTAGATCAAAAGTCTCTATTGTGACAGTACATGCCCTTTCATGAAATTCGAG 2503
Db 2420 GTAGTTGCTTACGAGCTCGGCTTGGTGGATACCCACAGCCATTTCTAAACCTAGAG 2479
Qy 2504 TTTGCTATGCAATCAGGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGA 2563
Db 2480 ATGATCTATGCAATCAGAATGACTTTAGGAAAACGGCACAGAAGCCGCTTCTTTCCAA 2539
Qy 2564 AGTAGCGGCTTGTGAATCTTGCCTTACCTATCGGATCCGATTTGATAGGAATCAGAC 2623
Db 2540 AGTGAAGACCTCTTCAATCTAGCGGTTCTCTGAGGGAATAAATTTGAGAA-----ATTC 2593
Qy 2624 TGCCAAAGTCAACGCTACAACTAACTCTTTGGTTATATCTGTGGATCTTGTTCGTAGTAAC 2683
Db 2594 TCCGATAAGTCTACGTATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAATGAT 2653
Qy 2684 CCCGCTGTATGCAACACCTCGGAATTAGCGGTGATTTCTTGGAAAACCTTCGGTACGAAT 2743
Db 2654 CCAGGCTGCACGACAACTCTTATGTTTCTTGGGGATTTCTTGGTGCACATGTGTACAAAGC 2713
Qy 2744 TTGGCAGACAGCTTTTAGTCTTCTGTCGAGGGAACCATTTTGTCTTAACTCAAAATTTT 2803
Db 2714 TTGCTTAGACAGAGCTCTTCTTGTACGTGCTGGAATCATCATGCTTTGCTTCAACTTTT 2773

Qy 2804 GAAGCTTTAGCCAAATTTCTTTTGAATTGCGTGGTCAATCTCGCAATTCATATGATGAC 2863
Db 2774 GAAGTTTTCACTAGTTTGAAGTCGAGTTGCGAGGTTCTTCTCGTAGCTATGCTATCGAT 2833
Qy 2864 TTAGAGCAAAATACCAATTTCTAATGC 2890
Db 2834 CTTGAGGAAGATTCCGATTTTAATCC 2860

RESULT 12
ID ABL91192 standard; DNA; 534 BP.
XX ABL91192;
XX AC
XX 29-AUG-2003 (revised)
DT 29-JUL-2002 (first entry)
XX
XX Chlamydia pneumoniae cp0014 ORF DNA, SEQ ID NO:18.
XX
XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CWL029; open reading frame; ORF; gene; ds.
XX
XX Chlamydia pneumoniae.
XX
XX Key Location/Qualifiers
CDS 1..534
FT /*tag= a
FT /product= "cp0014"
XX
XX WO200202606-A2.
XX 10-JAN-2002.
XX
XX 03-JUL-2001; 2001WO-IB001445.
XX
XX 03-JUL-2000; 2000GB-00016363.
PR 11-JUL-2000; 2000GB-00017047.
PR 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
PR 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
PR 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Ratti G, Grandi G;
XX
XX WPI: 2002-154726/20.
XX N-PSDB; ABB90534.
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
XX Claim 5; Page 49; 364pp; English.
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia

CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 534 BP; 147 A; 105 C; 117 G; 165 T; 0 U; 0 Other;

Query Match 17.4%; Score 523; DB 6; Length 534;
 Best Local Similarity 39.8%; Pred. No. 1.4e-134;
 Matches 534; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 101 ATGAAGTCTTCTTTCCCAAGTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 160
 Db 1 ATGAAGTCTTCTTTCCCAAGTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 60
 QY 161 ATTGCTACCGAGACAGTTTGGATTCAAGTGGGATTTCCGATGGGAATAAAATGGTAA 220
 Db 61 ATTGCTACCGAGACAGTTTGGATTCAAGTGGGATTTCCGATGGGAATAAAATGGTAA 120
 QY 221 TTTTTCAGTTCGTGAGTACGAGGAGTCTGGAAGTCTACCTATTTAAAGGGAATGTC 280
 Db 121 TTTTTCAGTTCGTGAGTACGAGGAGTCTGGAAGTCTACCTATTTAAAGGGAATGTC 180
 QY 281 ACTCTAGAAATATTCCTGGAAACAGGCACAGCAATCAAAAAAGCTCTTTTAAACAACACT 340
 Db 181 ACTCTAGAAATATTCCTGGAAACAGGCACAGCAATCAAAAAAGCTCTTTTAAACAACACT 240
 QY 341 AAGGGGATTTGACTTTACAGTAACGGGAATCTCTATTGTTCACAAAGTGGATGCA 400
 Db 241 AAGGGGATTTGACTTTACAGTAACGGGAATCTCTATTGTTCACAAAGTGGATGCA 300
 QY 401 GGGACTGTACGAGGCTGCTGTATACAGCAGCGTGTAGATAAATCTACAGTTTATA 460
 Db 301 GGGACTGTACGAGGCTGCTGTATACAGCAGCGTGTAGATAAATCTACAGTTTATA 360
 QY 461 GGGTTTTCTTCGCTATCTTTTATTGCTCTCTCGAAGTTTCGATACTACCGCAAGGA 520
 Db 361 GGGTTTTCTTCGCTATCTTTTATTGCTCTCTCGAAGTTTCGATACTACCGCAAGGA 420
 QY 521 GCGTTAGTCTCTACGGTAGCTTGAAGTTTGACAAAAATCTCAGTTTGTCTTTCAGC 580
 Db 421 GCGTTAGTCTCTACGGTAGCTTGAAGTTTGACAAAAATCTCAGTTTGTCTTTCAGC 479
 QY 581 AAAAACTTTTCAACGGTAATGCGGTGCTATCACCGCAAAACTCTTTCATTAA 635
 Db 480 AAAAACTTTTCAACGGTAATGCGGTGCTATCACCGCAAAACTCTTTCATTAA 534

RESULT 13

AA06821

ID AA06821 standard; DNA; 2757 BP.

XX AA06821;

AC AA06821;

XX 17-OCT-2003 (revised)

DT 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp9 DNA.

DE Omp9; outer membrane protein 9; surface exposed protein; antigen;

XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.

KW Chlamydia pneumoniae.

XX WO9858953-A2.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-DK000266.

XX 23-JUN-1997; 97DK-00000744.

XX

XX PA

XX PA

XX PI

XX DR

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(BIRK/) BIRKELUND S.
 (CHRI/) CHRISTIANSEN G.

Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

WPI: 1999-105610/09.

P-PSDB; AAW06822.

Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins.

Claim 6; Page 55-56; 115pp; English.

This DNA sequence codes for the novel 96.7 kDa surface exposed protein Omp9 (see AAW89422) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX04816-27) encoding Omp4-Omp15 proteins (see AAW89417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in the other, and encode polypeptides of about 89,6-100,3 kDa and about 56,1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 2757 BP; 770 A; 564 C; 642 G; 781 T; 0 U; 0 Other;

Query Match

Best Local Similarity 17.4%; Score 522.2; DB 2; Length 2757;

Matches 1424; Conservative 0; Mismatches 1153; Indels 90; Gaps 12;

QY 242 GAAGATGCTGGAACTACCTATTTAAGGGAATGCTCACTAGAAATATTCCTGGA 301

Db 160 GATGCTAGTGGACGACCTATATCTCGATGGGATGCTCGATA--AGCCAAGCAGGG 216

QY 302 ACAGGCACAGCAATCAAAAAAGCTGTTTAAACAACATAAGGGCGATTGACTTTTCA 361

Db 217 AAACAAACGAGCTTAACCAAGTTGTTTTCTAACACTGCAGGAATCTTACCTTTTA 276

QY 362 GGTACGGGAATCTCTATTGTTTCCAAACGGTGGATGCGAGGACTGTAGCGGGCTGCT 421

Db 277 GGGACGGATTTTCTCTCATTTTGACAATATTATTTCGTACTCTGTCAGGTGTTGT 336

QY 422 GTTACAGCAGCGTGTAGATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTT 481

Db 337 GTTACCAATACAGACTCTTGGGATTACGAATCTCAGGATTTTCAACTCTCGGATG 396

QY 482 ATTGGCTCTCTGGAAGTTTCGATACTACCGCAAGGAGCGGTAGCTGCTCTACGGGT 541

Db 397 CTTGACGCTCTT-----AGGACCACAGGTAAAGAGCCATTA--AAATTACCGAT 444

QY 542 ACCTTGAGTTTGACAAAAATCTCAGTTTGTCTTCAGCAAAAATCTTTCAACGGATAAT 601

Db 445 GGTCTGGTGTGAGAGTATAGGAATCTTGACCAAAATGAAATGTCCTTAGTGAAT 504

QY 602 GCGGTGTCTATCACCGCAAAACTCTTTCATTAAACAGGACTACAAATGTCAGCTCTGTT 561

Db 505 GGGGAGGCCATCAATACGAGACTTTGTCTTTGATGCGGAGTACGGGTTTGTAGCGTTC 564

QY 662 TCTGAAATACCTCTCTCAAGAAAGCGGAGCAATTCAGACTTCGATGCCCTTACCAT 721

Db 565 CTTGGCAATAGCTCGTCCCAACAGGGGAGGAGTCTATGCTTCTGGTACTCTGTGATT 624

QY	722	ACTGGAACCAAGGGAAGTCTCTTTTCTGACAAATCTCTTCGGATTCTGGAGCTGCA	781	QY	1793	ATGGGTGAGAAATTCATTAACGGCTATCAGGGAACTTGGGGCCCAATTTGTTGGGGACA	1852
DB	625	TCTGAGAATCAGGAATCTTGAGCTTCGGAACCAACAGTGCACAAATCAGAGGCGG	684	DB	1675	CTAAATACTACGAATCACTATGGGTATCAGGAACT---GGAATAATTTGTTGGGTCGAC	1731
QY	782	ATTTTTCAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTAATGCAAT	841	QY	1853	GGGCTTCT-----ACGACTGCAACCTTCAACTGACTTAAACTGGGTATATTCCT	1903
DB	685	ATCTCTGCTGAGGGAACCTTGATCTCCRAATACCAAAATATCTTTTTCGATGGCTGC	744	DB	1732	GATGCACTGCAAAAACAAAAATGCTACCTTAACCTTGACTTAAACAGGATACAAGCG	1791
QY	842	AAGTCAACAGGCGAGCTCTCAACAGGGGGATATGTCAGGAGGTGCTATCTGTGCT	901	QY	1904	AATCCGAGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATAT	1963
DB	745	AAAGCAACTCAAAATGGGGAGCTATTGATTGTAAACAAAGCAGGGG-----	790	DB	1792	AATCAGAACTCAGGACCTTTTGGTCTTAATAGCTTGGGGTCTTTTGTGCGATGTC	1851
QY	902	TATATACTAGTACAGATACTAAGGTCAACCTCACTCGGAATTCAGATGTACTCTTCAGC	961	QY	1964	AGCTCTCCATATCTTATGAGAGCTGCAACAGAGGGTTGCGAGGAGACCGTCTTTT	2023
DB	791	-----CGAACCCAGACCTTATCTTGACTCTTTTCAGGAATGAGGCTGCAATTTCTG	843	DB	1852	CGCTCAATCAGAGCCTCATGACCGGAGCAACAGTTCGTTATCTTCGTCACAAATTTG	1911
QY	962	AACATACTACACACAGCGGGAGAGCTATCTATGTGMAAAAGCTCGAATGCGCTGCC	1021	QY	2024	TGCTGTGCTGATATCTAACTTCTCCATAAGGATAGTACAAAAACACGACGCGGTTT	2083
DB	844	AATAACACAGAGGAATAGTGGAGTGCATTTATACCAAAATTTGGTGTATCTCTCA	903	DB	1912	TGGGTATCAGGAATCGCGACTTTTTCATGAGATCAGAAAGGAAACCAAGTAGTAT	1971
QY	1022	GGAGACTTACCTTATTCAGTAGAATAGTGTCAATGGAGGTACAGCTCTTAAGGTGGA	1081	QY	2084	CGCCATTTGAGTGGCGTTATGTCTATAGGAGGAAAACCTACATPACTTGTTCAGATAAGAT	2143
DB	904	GGACGAGGAGGAGTGTATTTTCTAACCAACAAAGCTGCGAATGCTACTCTTAAGAGGG	963	DB	1972	CGTCATTTAGCGCGGTTATGCAATAGGAGGAGTCTTTCACGGCTTCGAAAAATTC	2031
QY	1082	GCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCGCCGATAGTGGTGACATTTGC	1141	QY	2144	CTTAGTGTGCAATTTTGTGAGCTCTTTTGAAGAGATAGAGTACTTTGTAGCTAAGAT	2203
DB	964	GCAATTCGATCTAGATCTTGAGAGATAGCAATTTCTGCAGATCTCGGCAATATCAT	1023	DB	2032	TTTAATTTTGTCTTTTGTGAGCTTTTGTGCTACGACAGGAGCCTCTTGTGGCTAAGAC	2091
QY	1142	TTTTTAGGGAATPACAGTCTCTTAC-----TACTCTGGGACCAATAGAGTAGTATC	1195	QY	2204	CAAGGTACAGTCTACGGAGGAACTCTTATTTACACAGCACAAACCACTATATCTCTTT	2263
DB	1024	TTTCGAGGGCAATACTACGAGCACTACAGGAAGTCTCTCGAGTGTGACCAAAATGCTA	1083	DB	2092	CATACCCATGTAATGAGGGGCAATGATTTACCGACACTCGGAGAGTCTAAGACCTC	2151
QY	1196	GACTTAGGAACGAGTGCAAGATGACAGCTTTGCGTCTGCTGCTGGTAGGCCATCTAC	1255	QY	2264	CCTTGCAAACTACGGCCTTTGTTGTTTGTATGTTCTCTACAGAGATTCCTGTTCTCTTT	2323
DB	1084	GATCTGCAATGCAAAATTTTAAATCTCCGAGCGACTCGGGGAAATAAAGTTATT	1143	DB	2152	GCTAAGA-----TTTTGTGAGGAATTTCTGACTCCCTACTTTTGTCTTC	2196
QY	1256	TTCTATGATCCCATACTACAGGATCATCCACACAGTTTACAGATGCTCTTAAAGTTAAT	1315	QY	2324	TCAGAAACCTTAGCTACACCCATACGATACAGTCTGAAACCAAGTATACAATAT	2383
DB	1144	TTCTATGATCTTATACGA-----GCTCAGGAGTACTGATAAGCTCTCTTTGAAT	1194	DB	2197	AATGTCGGTGTGCTTATGGCCATACCGACAATAACATACCACAAAGTACACTGGCTAT	2256
QY	1316	GAGACTCCGGCAGATTTCTGCATACAAATATACAGGGAACATCATCTTTCACAGAGAAAG	1375	QY	2384	CCTACTGTTTAAAGGAAGCTGGGGATGATAGTTTCGCTTTAGAAATTCGGTGGAGAGCT	2443
DB	1195	AAAGCTGACGAGGATCTGGAATACCTATGAAGCTACATCGTTTCTCTGAGAGAAA	1254	DB	2257	TTCTCTGTTTAAAGGAAGCTGGGGAATGATGCTTCGGTATAGAAATGCGAGGAGCTATC	2316
QY	1376	TTATCAGACACAGAGCCCGAGATTTCAAATCTTACTTCGAAGTACTACAGCCTGTA	1435	QY	2444	CCGA---TTTGTCTTAGATGAAAGTGTCTATTTGAGCAGTACATGCCCTTCATGAAATG	2500
DB	1255	CTCTCAGAGAGGAACCTTAAGAAACCTGCAATCTGAAAGTCTACATTTTACAGGCTGTA	1314	DB	2317	CCGAGTGTGCTTCAGGAGCTCGGTCTTGGTGGATACCCACACGCAATTTCTAAACCTA	2376
QY	1436	ACTCTTTTCAGGAGTACTCTATCTTTAAACATGAGTGAATCTGCAGACTCAGGCAATTC	1495	QY	2501	CAGTTTGTCTATGCACATCAGGAAGTTTAAAGACAGGGAACAGAGCTCGTGAATTT	2560
DB	1315	GAGCTTCTGCAGTGCCTTAGTATTTGAAGATGGAGTGAATGCTAGTTGCAATATCTATA	1374	DB	2377	GAGATGATCTATGCACATCAGAAATGACTTTAAGGAAAACGGCAGAGCGGCTCTTTC	2436
QY	1496	ACTCAACAGCGAGATTTCTGCTCGAAATGGAGTGAAGTACTACTCTAGA---ACCTGCT	1552	QY	2561	GGAAGTACGCGCTTGTGATCTTGCTTACCTTACCTATCGGGATCCGATTTGATAGGAATCA	2620
DB	1375	ACGAGCTCGAGGATCGAAAGTCGTTATGATGAGGAGGACTACTTTTGGGCAAGCGCT	1434	DB	2437	CAAAGTGAAGACCTCTTCAATCTAGCGGTTCCTGTAGGGATAAAAATTGAGAA-----A	2490
QY	1553	GATACTAGCACCATAACAAATTTGGTCATTAACATCAGTTCTATAGACGTGCAAGAGAG	1612	QY	2621	GACTGCAAGATGCAACGTFACAAATCTTAACTCTTTGGTTTACTTGTGATCTTGTTCGAGT	2680
DB	1435	GAGGGGTCACTCTCAATGGCCATAGCCATTAATAGATTTCTTATGATGGGCAATATAA	1494	DB	2491	TTCTCCGATAAGTCTACGTATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAAT	2550
QY	1613	GCAAAATAGAAACCAAGCTAGCTCAAAATATCTGACTTTTATCTGGAACCATCACTTTA	1672	QY	2681	AACCCGACTGTACGACAACTCGCAATTAGCGGTGATTTCTTGAAAACCTTCGGTAGC	2740
DB	1495	GCTATCATTAAGCGGACGAGCAAGTAAGGATTTGCCCTTATCAGGGCCTATCATGCTT	1554	DB	2551	GATCCAGGTGACGACAACTCTTATGGTTTCGGGGATTTCTGGTGCACATGTTGATCA	2610
QY	1673	TTGACCCGACGCGCGCTTTTATGAAAATCATAGTTTAAAGAAATCTCTAGTCTTAGCAC	1732	QY	2741	AATTTGGCAAGCAAGCTTTTAGTCTTCCTGTCAGGGAACCAATTTTGTCTTAACTCAAAAT	2800
DB	1555	GTAGATGCTCAGGGGAATATTATGAGCATATAATCTCAGTCAACAGCAGGCTTTTCCCT	1614	DB	2611	AGCTTGTCTAGACAACTCTTCTTGTACGTGCTGGAATCATCATGCTTGTCTCAAAAC	2670
QY	1733	ATCTTAGAGCTCAAGCTCTCGAATCTGAACGTGAACAGACCGCAGTGAATCCAGATCTTATA	1792	QY	2801	TTTGAAGCCTTTTAGCCAAATTTTCTTTTGAATTCGGTGGGTGCTCTCGCAATTTACAATGA	2860
DB	1615	TTAATAGAGCTTTCTGCAAGGACGATGACTACTACAGATATCCCGGATACCCCAATT	1674	DB	2671	TTTGAAGTTTTCAGTCAGTTTGAAGTCGAGTTCGAGGTTTCTTCTCGTAGCTATGCTATC	2730
				QY	2861	GACTTAGGACAAAATACCAATTTCTAA	2887

Db2731GATCTTGGAGGAAGATTTCGATTTTAA2757

RESULT 14

AAx91990_05

Continuation (6 of 13) of AAx91990 from base 500001 (Nucleotide sequence of the complete sequence split into 13 fragments) LOCUS AAx91990 Accession AAx91990

Fragment Name	Begin	End
WP AAx91990_00	1	110000
WP AAx91990_01	100001	210000
WP AAx91990_02	200001	310000
WP AAx91990_03	300001	410000
WP AAx91990_04	400001	510000
WP AAx91990_05	500001	610000
WP AAx91990_06	600001	710000
WP AAx91990_07	700001	810000
WP AAx91990_08	800001	910000
WP AAx91990_09	900001	1010000
WP AAx91990_10	1000001	1110000
WP AAx91990_11	1100001	1210000
WP AAx91990_12	1200001	1230025

Query Match

17.3%; Score 518.4; DB 2; Length 110000;

Best Local Similarity 52.8%; Pred. No. 3.6e-132;

Matches 1403; Conservative 0; Mismatches 1201; Indels 60; Gaps 11;

QY	250	TGGAACCTACCTACTATTAAAGGGAATGTCACTCTAGAAAATATTCTCGAACACGGCAC	309
DB	7879	TGGAACGAACATGTCTTATCAGGAATGTCTATATAACGA---TGCTGGGAAGGCAC	7935
QY	310	AGCAATCAAAAAGCTGTTTTAACACATAAGGGCGATTTCAGCTTTCACAGGTAAACGG	369
DB	7936	AGCATTAAACAGGCTGCTCTTTACAGAAACTACGGGTGATCTGACATTTACTGGAAGGG	7995
QY	370	GAATCTCTTAATGTTCCAAACGGTGGATGCAGGACTGTAGCAGGGGCTGCTGTTAACAG	429
DB	7996	ATACTCATTTTCATTCAACACGGTAGTACGGGTTCGAATGCAGGAGCTGCGG---CAAG	8052
QY	430	CAGCGTGTAGATAAATCTACCACTGTTTATAGGTTTCTTCGCTATCTTTTATTCGGTC	489
DB	8053	CACAACCTGCTGATAAAGCCCTTAACATTCACAGGATTTCTTAACCTTTCTTCATTGCAGC	8112
QY	490	TCTTGGAGTTTCATTAACCTACCGGAAAGAGCGGTTAGCTGCTCTACGGGTAGCTTAG	549
DB	8113	TCTCTGAACCTACAGTTGCTTCAGGAAAAGTACTTTAA---GTTCTGCAGGAGCCTTAA	8169
QY	550	TTTGACAAAAAATGTCTAGTTTGTCTTTCAGCAAAAACCTTTTCAACGG-----ATAA	600
DB	8170	TCCTACCGATATGGAACGATTCCTTTAGCCHAAACGCTCCAAATGAAGCTAATAACAA	8229
QY	601	TGCGGTGTCTATCACCAGCAAAAACCTCTTTCAATTAACAGGAGCTACAAATGCAGCTCTGT	660
DB	8230	TGCGCGAGCGATCACCGCAAAAACCTCTTCTAATTCGGAATACCTCTTCTATAACCTT	8289
QY	661	TTCTGAAATACCTCTCTAAAGAACGGAGCCATTACAGCTTCGATGCCCTTACCAT	720
DB	8290	CACCTAGTAATAGCGCAAAAATAATAGGTGAGAGCATCTATAGCTCTCGCGCTGCAAGTAT	8349
QY	721	TACTGGAACCAAGGGAAGTCTCTTTTCTGACATACTTCTTCGATTCTTCGAGCTGC	780
DB	8350	TTCAGGAACACCGGCGAGTTAGTCTTTATGAATAATAAGGAGAACTCGGGGGTGGGGC	8409
QY	781	AATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCTCTTTATTGACAA	840
DB	8410	TCTGGGCTTTGAAGCGAGCTCTCTCGATTACTCAAAATAGCTCCCTTTCTCTCTGGAAA	8469
QY	841	TAGGTCACAGGAGCGAGCTCCCAACACGGGGGATATGTCAGGAGGTGCTATCTGTGC	900
DB	8470	CACCTGCAACAGATGCTGCAGGCAAG-----GGCGGGGCCATTATTG	8511
QY	901	TTATAAACTAGTACAGATACTAAGGTCAACCTCAGTGGAAATCAGATGTTACTTTCAG	960

QY 2026 GTGTCTGGATTAATCTAACTTCTTCCATAAGATAGTACAAAAACACGACGCGGTTTCG 2085
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QY 2086 CCATTGTAGTGGCGGTTATGTCTATAGGAGGAACCTACATATCTTCTCAGATAAGATTCT 2145
Db 9709 ACATAAAGCTACGCTATATTTGTGGAGGAGTCTGAAGATTCTTCTGAAATATCTT 9768
QY 2146 TAGTCTGCAATTTGTAGCTCTTTGGAGAGATAGAGACTTCTTTGTAGCTTAAGAAATCA 2205
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QY 2266 TTGCAAACTACGCGCTTGTTCGTCTTATGTCTTCTACAGAGATTCCTGTTCTCTTTTC 2325
Db 9886 TCCCATGCCCTCATTTTGAAGTATCACCGACATGCTGAAAGATATTCCTCTCATTTTGA 9945
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QY 2386 TACTGTATAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGGGAAGA---GC 2442
Db 10006 TGAGCTCAAGGCTCTTGACCAATTAATCTCGGGCTCTAGAGCTCGGAGGATCTCTGC 10065
QY 2443 TCCGATTTGCTTAGATGAAGTGTCTTATTTAGCAGATGATACGCTTCTCATGAATGCA 2502
Db 10066 TCTATATCTCCCTAAAGAGCACCGTTCTTCCAGGATATTTCCCTTCTTAAAGTTCCA 10125
QY 2503 GTTGTCTATGACATCAGGAGGTTTAAAGACAGGAGCAAGAGCTCGTAATTGCG 2562
Db 10126 GGCAGTCTACGCGGCCAACAAACTTTAAAGAGAGTGGCGCTGAAGCCCGTCTTTGA 10185
QY 2563 AGTAGCCGTCTGTGAATCTTCCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGA 2622
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QY 2803 TGAAGCCTTTAGCAATTTCTTTTGAATTTGCGTGGTCTATCTGCAATTTACATGTAGA 2862
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Db 10486 TTGTGGCTAAGATACTCAATCTAGTTCCT 10515

RESULT 15

AAA30851

ID AAA30851 standard; DNA; 2950 BP.

XX AC

XX AC

DT 15-SEP-2003 (revised)

DT 29-AUG-2000 (first entry)

XX Chlamydia antigen CPN100638 full length coding sequence.

XX

KW Chlamydia antigen; diagnosis; infection; community acquired pneumonia; therapy; upper respiratory tract disease; bronchitis; sinusitis; asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma; ds.
KW Chlamydia pneumoniae.
OS Key Location/Qualifiers
FH 101..2887
FT /tag= a
FT /product= "Chlamydia antigen CPN100638"
XX WO200032794-A2.
XX 08-JUN-2000.
XX 01-DEC-1999; 99WO-CA001147.
XX 01-DEC-1999; 98US-0110339P.
PR 01-DEC-1999; 98US-0110340P.
PR 01-DEC-1999; 98US-0110427P.
PR 01-DEC-1999; 98US-0110428P.
PR 01-DEC-1999; 98US-0110438P.
XX (CONN-) CONNAUGHT LAB LTD.
XX Murdin AD, Oomen RP, Wang J;
PI WPI; 2000-412339/35.
XX P-PSDB; AAY90239.
XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for preventing, diagnosing and treating diseases such as community acquired pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset asthma.
XX Claim 2; Fig 5; 174pp; English.
XX This sequence encodes a Chlamydia antigen of the invention, designated CPN100638. The nucleic acids (and their complementary sequences) may be used as diagnostic agents for detecting the presence of nucleic acids encoding Chlamydia antigens in samples according to standard methods, and therefore, for diagnosing Chlamydia infections. For example, they may be used as primers and probes for diagnostic polymerase chain reaction (PCR) assays. Antisense sequences may be used to down regulate expression of the proteins and may be used to treat infections. The nucleic acids may also be used to produce the protein antigens they encode according to standard recombinant DNA methodologies. The proteins may then be used as antigens for the production of antibodies (i.e. as vaccines) for preventing infection by Chlamydia. The antibodies may also be used as diagnostic reagents for detecting infections. Chlamydia is a pathogen implicated in the development of (for example) community acquired pneumonia, upper respiratory tract disease (especially bronchitis and sinusitis, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults. (Updated on 15-SEP-2003 to standardise OS field)
XX Sequence 2950 BP; 855 A; 724 C; 562 G; 809 T; 0 U; 0 Other;

Query Match 17.3%; Score 518.2; DB 3; Length 2950;
Best Local Similarity 53.3%; Pred. No. 7e-133;
Matches 1427; Conservative 0; Mismatches 1173; Indels 75; Gaps 13;

QY 243 AAGATGCTGGAATCTACCTATTTAAGGGAATGTCTAGAAAATATTTCTTGAA 302
Db 258 ATGCAGATGGAATCTATCTATAATCTAACAGGGATGTCTC---AATCACAATGCAGAT 314
QY 303 CAGGCACGCAATCACAAGAGTGTTTTAAACACACTAAGGGCGATTTCATTTCCAG 362
Db 315 CTCGACAGCTCTAACCGCTTCTCTGCTTTTAAAGAACTACTGGAAATCTTCTTCCAG 374
QY 363 GTAACGGGAATCTCTTATTTTCCAAACGGTGGATGCAGGACTGTAGCAGGGGTGTG 422

Db 375 GCCAGCGGTACCAATTTCTCCTCAAAAATATCGATGCGGG-----AGCGAACTGTACCT 428
Qy 423 TTACAGCAGCGTGTAGATAAAUCTACACAGTTTATAGGGTTTTCCTGCTAICTTTTA 482
Db 429 TTACCAATACAGCTGCAAAATAGCTTCTCTCTTTTCAGGATTCCTCTATTGTGCACTAA 488
Qy 483 TTGGGTCTCTCGAAGTTCGATAACTACCGGCAAGAGCGGTAGCTGCTCTACGGGTA 542
Db 489 TACAAACCAACGAATGCT-----ACCACAGGAACAGGAGCCATCAAGTCCACAGAGCTT 542
Qy 543 GCTTGAAGTTGACAAAAATGTGAGTTTGTCTTCCAGCAAAAACCTTTTCAACGGATAATG 602
Db 543 GTTCTATTCACTCGAACTAT---AGTTGCTACTTTTGGCCAAAACCTTTTCTAATGACAAATG 599
Qy 603 GCGGTGCTATCAGCGCAAAACTCTTTTCATTAAACAGGAGCTACAAATGTGCTGCTGTTTT 662
Db 600 GAGGCGCCTCAAGGCGAGCTCTATCAGTCTATCGCTAAACCCCAACCTAAC--GTTTG 656
Qy 663 CTGAAAATPACCTCTCAAGAAAGGCGGAGGCAATTCAGACTTCGGATGCCCTTACCAATTA 722
Db 657 CCAAAAACAAAGCAACGCAAAAAGGGGTGCCCTTATTCACGGGAGGATTAACAATTA 716
Qy 723 CTGGAACCAAGGGAAGTCTCTTTTCTGCAATATCTTCTTCCGATTCCTGGAGCTGCAA 782
Db 717 ACAATACGTTAAACTCAGCATCATTTTCTGAAAATACCGCGCGCAACAAATGGCGAGCCA 776
Qy 783 TTTTTCAGAAAGCCTCGGTGACTATTTCTAATAATGCTAAGTTTCTTTTATTCACRATA 842
Db 777 TTTTACAGGAAGCTAGCAGTTTATAGCAGCAACAAAGCAATTAGCTTTTATAAACAAATA 836
Qy 843 AGGTACAGGAGCGAGCTCTCAACAAAGGGGGATATGTACAGGAGTGTCTATCTGTGCTT 902
Db 837 GTGTGACCG-----CAACCTCAGCTACAGGGGGAGCCATTTACTGTAGTA 881
Qy 903 ATAAAACTAGTACAGATCTAAGGTACCCCTCACTCGGAATCAGATGTACTCTTCAGCA 962
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Qy 963 ACAATACATCAGAACACGGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTCCG 1022
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Qy 1083 CCATAGCTATCGAAGATAGTGGGAATAGTTTATCCGCGATAGTGGTGACATGTCT 1142
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Qy 1311 TTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTACAGAG 1370
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Qy 1371 AAAAGTTATCAGACAGAGCCGAGATTCTTAAAAATCTTACTTCGAAGCTACTACAGC 1430
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Db 1422 CTCTAACTCTTGGGGAGGGCAACTCTCTCTTAAATCAGGAGTCACTCTAGTTGCTAAGT 1481

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Qy 1551 CTGATACTAGCACCATAAACAAATTTGGTTCATTAACATCAGTTCTATAGACGGTGCAGAGA 1610
Db 1542 CTGATGGATCACTATCAATAATCTTGTTCATATGTAGATTCCTTAAAGAGACCAAGA 1601
Qy 1611 AGGCAAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTTATCTGGAACCACTCACTT 1670
Db 1602 AGGCAACGCTAAAAAGCAACCAAGCAAGTCAGACAGTCTTATCTGATCGCTCTCTC 1661
Qy 1671 TATTGGACCGGACCGGCGAGCTTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCTTACG 1730
Db 1662 TTGTAGATCTCTTCTGGAATATGCTACGAAGATGTCTCTTGAATAAACCTCAAGTCTTTT 1721
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Qy 1899 TTCTTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGAAATCATTATTAG 1958
Db 1902 ATCGAATCTGAGCGTCTGGAACTTGTGTGTAACACGCTATGGGATCTCTTTGTTG 1961
Qy 1959 ATATTAGCTCTCTCCATTTATCTTATGGAGACTGCAAAACGAAGGGTTGCAGGAGACCGTG 2018
Db 1962 ATGTGCGCTCCATACAAACAGCTTGTGCCACTTAAAGTAGCCCAATCTCAAGAAACTCGC 2021
Qy 2019 CTTTTTGGTGTGCTGGATTATCTAACTTCTTCATAGGATAGTACAAAACACAGACGG 2078
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Qy 2496 AATTGCAAGTTTGTATGCACATCAGGAAGGTTTTTAAAGAAC---AGGGAAACAGAAAGCTC 2552
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Db	2613		
QY	2673	TTCCGTAGTAAACCCGACTGTACGCAACAACACTCGGAATTAGCGGTGATCTTTGAAAAACCT	2732
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QY	2733	TCGGTACGAATTTGGCAAGCAAGCTTTAGTCTTCGTCAGGGAACCAATTTTGTCTTAA	2792
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QY	2793	ACTCAAAATTTGAAGCTTTAGCCAAATTTCTTTGAATTTGGTGGTCACTCTCGCAATT	2852
Db	2793		
QY	2853	ACAAATGACTTAGGAGCAAAATACCAATTTCTAA	2887
Db	2853		

Search completed: August 16, 2004, 15:10:01
Job time : 793 secs

Tue Aug 17 09:45:49 2004

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 12:57:47 ; Search time 4916 Seconds

(without alignments)
18223.463 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

Sequence: 1 cgccttacttagtaggt.....tggtttgctaaacacttcc 3000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:**

2: em_esthum:**

3: em_estin:**

4: em_estmu:**

5: em_estcov:**

6: em_estpl:**

7: em_estro:**

8: em_htc:**

9: gb_est1:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pln:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_pbg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51.8	1.7	409	29	CE143861 tigr-gss-
C 2	50.6	1.7	923	29	AL105699 Drosophil
C 3	49.4	1.6	334	9	AU076383
C 4	46.8	1.6	585	9	AU263143

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	46.8	1.6	1201	13	BX336919
6	46.2	1.5	853	10	BF265090
C 7	45.4	1.5	843	28	BZ643413
C 8	45.4	1.5	1201	13	BX376097
C 9	44.8	1.5	391	9	AU263574
C 10	44.8	1.5	720	29	AG088699
C 11	44.6	1.5	592	28	AZ972038
C 12	44.4	1.5	1025	29	CNS014J2
C 13	44	1.5	450	12	BM881804
C 14	44	1.5	498	12	BG602722
C 15	44	1.5	593	12	BG602721
C 16	44	1.5	735	12	BM160527
C 17	44	1.5	767	12	BM657645
18	43.8	1.5	596	29	FR0019514
19	43.8	1.5	820	28	BM051138
C 20	43.6	1.5	574	28	AZ526815
21	43.6	1.5	1354	29	CG744717
22	43.2	1.4	716	12	BM627037
23	43.2	1.4	1101	29	CNS008VI
C 24	43.2	1.4	1201	13	BX394744
C 25	42.8	1.4	783	29	CNS00A1S
26	42.8	1.4	795	14	CF288665
27	42.8	1.4	1201	29	CNS0167M
C 28	42.6	1.4	1177	13	BX338151
C 29	42.4	1.4	240	9	AU072820
C 30	42.4	1.4	1101	29	CNS00039G
C 31	42.2	1.4	660	28	AZ567761
C 32	42	1.4	900	28	AQ744776
C 33	42	1.4	1201	13	BX337161
34	41.8	1.4	516	10	BF954368
C 35	41.8	1.4	712	13	BX416727
C 36	41.8	1.4	998	13	BX436885
37	41.6	1.4	509	12	BM316139
38	41.6	1.4	553	9	AW019090
39	41.6	1.4	1101	29	CNS00KF8
40	41.4	1.4	480	28	BZ643398
41	41.4	1.4	926	28	BH156551
C 42	41.4	1.4	948	13	BX414840
C 43	41.4	1.4	1101	29	CNS017NE
44	41.4	1.4	1201	13	BX384793
C 45	41.4	1.4	1214	14	CK211400

ALIGNMENTS

RESULT 1	CE143861	409 bp	DNA	linear	GSS 25-SEP-2003
LOCUS	tigr-gss-dog-17000371268042	Dog Library	Canis familiaris	genomic,	
DEFINITION	genomic survey sequence.				
ACCESSION	CE143861				
VERSION	CE143861.1				GI:35256524
KEYWORDS	GSS.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
AUTHORS	1 (bases 1 to 409) Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.				
TITLE	The dog genome: survey sequencing and comparative analysis				
JOURNAL	Science 301 (5641), 1898-1903 (2003)				
MEDLINE	22875432				
PUBMED	14512627				
COMMENT	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirknes@tigr.org				

FEATURES	source	Class: shotgun.	Location/Qualifiers
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			/strain="Standard Poodle"
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			/clone_lib="Dog Library"
			/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
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Best Local Similarity		53.1%;	Pred. No. 0.048;
Matches 110;	Conservative	0;	Mismatches 97; Indels 0; Gaps 0
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Db	155	AGTCCAAATTATCAATATTAGATCATGCCCTTGATGTACTAAACACATAAAATAAATA	214
QY	83	CAAAGTATATATTTACAANTGAAGTCTCTTTCCCAAGTTGTATTTTCTACATTTGCT	142
Db	215	GAATGTCATTACTATACCCAGTGCCTAGTTTCTATACCACATTATTTTGTAGTTTGA	274
QY	143	ATTTCCCTTTGCTATGATGTCTACCGACAGCTTTTGGATTCAAGTGGCAGTTTCAT	202
Db	275	ATTTACATATATCTATGATCTATTTTGAGTTAAATTTTGTGAAGGTACAAAGTGTTA	334
QY	203	GGGAATAAAANTGGTAATTTTTCAGTT	229
Db	335	GGTAAGTAACTGAACTCTTTTCTTTT	361

RESULT 2	CNS01509	923 bp	linear	GSS 26-JUL-1999
LOCUS	Drosophila melanogaster	genome survey	sequence SP6	end of BAC
DEFINITION	BAC114820 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL105699			
VERSION	ALI05699.1	GI:5617836		
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 923)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
COMMENT	- Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.			

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FEATURES
    source
        Location/Qualifiers
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Query Match 1.7%; Score 50.6; DB 29; Length 923;

[illegible]

RESULT 3	ACCESSION	REFERENCE
AU076383/c	VERSION	AUTHORS
LOCUS	KEYWORDS	TITLE
DEFINITION	SOURCE	JOURNAL
	ORGANISM	COMMENT

AU076383 334 bp mRNA linear EST 27-JUL-1999
 AU076383 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
 discoideum cDNA clone SSA686, mRNA sequence.
 AU076383
 AU076383.1 GI:5607281
 EST.
 Dictyostelium discoideum
 Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 1 (bases 1 to 334)
 Urushihara, H.
 Developmental cDNA in Dictyostelium discoideum (1999)
 Unpublished (1999)
 Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp
 PROJECT = Dictyostelium discoideum cDNA project in Japan.
 Location/Qualifiers
 1. 334

FEATURES
source

ORIGIN
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"

```
Query Match      1.6%; Score 49.4; DB 9; Length 334;
Best Local Similarity 48.1%; Pred. No. 0.19;
Matches 140; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy    29   TTTCTTGACTGTTTCTTCCTATGGTGTAATCTCTAAATAATATAAATTCAAAATCAAAGT 88
Db    325  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 89 ATATATTTTACAAATGAGTCTCTTTCCCAAGTTTGTATTTTCTACATTTGCTATTTTC 148
Db 265 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 206

QY 149 CTTTCTCTATGATTCGTACCGAGACAGTCTTTGGATTCAAGTCGAGTTTTCGATGGGAAT 208
Db 205 CTATTTTTCAGATATTTCTGTACACCTTTATYAGATTCGAAATGTTCTTTCAAAGATCT 146

QY 209 AAAAATGGTAATTTTTCAGTTCGTGAGATCGAGAAAGATGCTGGAACACTACCTACCTATTT 268
Db 145 AAATGTGGGAACCTTACCATTGTATAGAGATCAGCAGCAAAATGTTAAACATAACCAATG 86

QY 269 AAGGAAATGCTACTAGAAATATTTCTCGACAGGACAGCAATCACA 319
Db 85 TATTCAAGCAACATAAACAATATAATCAGCAAAAGTGTAAAGATTTACCA 35

RESULT 4
AU263143/c
LOCUS AU263143 VS Dictyostelium discoideum cDNA clone VSE486 3', mRNA
DEFINITION
ACCESSION AU263143
VERSION AU263143.1 GI:20519690
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 585)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
JOURNAL stages of Dictyostelium discoideum
COMMENT Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
1..585
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSE486"
/sex="mat A"
/dev_stages="vegetative"
/clone_lib="VS"

ORIGIN
Query Match 1.6%; Score 46.8; DB 9; Length 585;
Best Local Similarity 47.9%; Pred. No. 0.96;
Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 38 TTGTTTCTCCATGTTGGTGTATCTCTTAAATATTTAAATCAAAATCAAAAGTATATATTTT 97
Db 584 TTGTTGTTGTTGTTGTTTACCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 525

QY 98 ACAATGAAGTCTTCTCCCAAGTTTGTATTTTCTACATTTGCTATTTTCCCTTGTCT 157
Db 524 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 465

QY 158 ATGATTTGTCACGACAGTCTTTCGATTCAGTGGAGTTTTCGATGGGAATCAAAATGCT 217
Db 464 AGATATTCGTACACCTTTATTTAGATTCGAAATGTTCTTCAAGAAATCTAAATGCTGGG 405

QY 218 AATTTTTCAGTTCGTGAGAGTCCAGGAATGCTGGAAGTACCTACCTATTTTAAAGGGAAT 277
Db 404 AACTTACCATTTGATATAAGAGATCACAGCAAAATGTTAAACATAACCAATGTTATTCATAA 345

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QY 278 GTCACTCTAGAAATATTTCTCTGGAACAGGCACAGCAATCACA 319
Db 344 GCAACATAACATATTAATCAAGCAAGTGTAAAGATTTACCA 303

RESULT 5
BX336919
LOCUS BX336919 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD10333YL20 5-PRIME, mRNA sequence.
ACCESSION BX336919
VERSION BX336919.1 GI:30345558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2019.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD10333DF10QPI&cluster=2019.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSOD10333DF10QPI.

FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD10333YL20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 1.6%; Score 46.8; DB 13; Length 1201;
Best Local Similarity 39.4%; Pred. No. 1.1;
Matches 85; Conservative 36; Mismatches 95; Indels 0; Gaps 0;

QY 14 TAGAGTTGAGTGAATTTCTTGACTTCTCTCTCTATGTTGGTGTATCTTAAATATATAA 73
Db 846 WATWBBTITTTTAAWTTWTTTWTWTTTITTTTTTTTTTTTACCTTTTAAAAAATAAA 905

QY 74 ATTCAAATCAAGTATATATTTTACAATGAAGTCTCTTTCCCAAGTTTGTATTTTCT 133
Db 906 ATWATWAWWAAATWTTTITTTTTTTTTTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 965

QY 134 ACATTTGCTATTTTCCCTTTGCTCTATGATTCGTACCGAGACAGTTTGGATTCAGTGGC 193
Db 966 TTTTITTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1025

QY 194 AGTTTCGATGGGAATATAAATGGAATTTTTCAGTT 229
Db 1026 ATTAATAAATTTTTTTTWWHTTTTTTTTTTTTTTTTTTTT 1061

RESULT 6
BF265090/c
LOCUS BF265090
DEFINITION HV_CEA0011D22f Hordeum vulgare seedling green leaf EST library

```

HVCNA0004 (Blumeria challenged) Hordeum vulgare subsp. vulgare
 cDNA clone HV_CEA0011D22f, mRNA sequence.
 BF265090
 BF265090.3 GI:163334636
 EST.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 853)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
 Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, J., Simmons, J.,
 Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Blumeria infected incompatible (Mla13)
 seedling leaf cDNA library
 Unpublished (2001)
 On Nov 17, 2000 this sequence version replaced gi:13261889.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 280
 Seq primer: AATAACCTCTACTAAAGGG
 High quality sequence stop: 831.
 Location/Qualifiers
 1..853
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="C16155 (Mla13)"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HV_CEA0011D22f"
 /tissue_type="seedling green leaf"
 /lab_host="TJC121"
 /clone_lib="Hordeum vulgare seedling green leaf EST
 library HVCNA0004 (Blumeria challenged)"
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 C.I. 16155 (Mla13) plants were greenhouse grown in the R
 wise lab at Iowa State University, Ames, IA; 7 day old
 green seedlings were challenged with isolate A27
 (AvrMla13) of Blumeria graminis f. sp. hordei, and leaves
 were harvested 20 and 24 hr post-inoculation and snap
 frozen; uninoculated leaves were harvested 20 hr
 post-inoculation (Wei, Wise). In the TJ Close lab at the
 University of California, Riverside, total RNA was
 prepared from each sample pool, equal quantities of all
 three RNA pools were combined, poly(A) RNA was purified
 from the mixture, one cDNA library was made, and 1 million
 pfu were in vivo excised to give pBluescript SK(-) cDNA
 phagemids (Choi, Close). Phagemids were plated and picked
 at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
 Oates, Rambo, Main). The sequence has been trimmed to
 remove vector sequence and contains a minimum of 100 bases
 of phred value 20 or above. For more details on library
 preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

Query Match 1.5%; Score 46.2; DB 10; Length 853;
 Best Local Similarity 57.8%; Pred. No. 1.4;

ORIGIN

Matches 78; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 29 TTCTTGTACTTGTTCCTCATTATGGTGTATCTCTTAAATATTAATAATCAAAATCAAGT 88
 |||||
 Db 808 TTTTATTTATTTGTTTAAATATNTAGTTTATATTTTAAAGTTGTTATTTTATT 749
 |||||
 QY 89 ATATATTTTACAATGAAGTCTCTCTTCCCAAGTTTGTATTTTCTCAATTTGCTATTTTC 148
 |||||
 Db 748 ATNTTTTGTGCGAAATTTTATTTTATTAAGTTTATTTTATTTTATTTTATTTTTC 689
 |||||
 QY 149 CCTTGTCTATGATT 163
 |||||
 Db 688 CTTTATCTATATTT 674
 |||||

RESULT 7
 BZ643413/c
 LOCUS
 DEFINITION
 BZ643413
 BZ643413
 BZ643413.1 GI:28104915
 GSS.
 SOURCE
 Zea mays
 Zea mays
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 843)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other GSSs: OGA057TC
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
 1..843
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBMA011J17"
 /clone_lib="ZM 0.7 1.5 kb"
 /note="Vector: pBGSK; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

FEATURES
 source
 1..843
 Query Match 1.5%; Score 45.4; DB 28; Length 843;
 Best Local Similarity 49.8%; Pred. No. 2.3;
 Matches 115; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
 QY 692 GCCATTGAGACTTCGATGCCCTTACCAATTACTGGAACCAAGGGAAGTCTCTTTTCT 751
 |||||
 Db 552 GCTACTGCTGCTGCTGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTACTACT 493
 |||||
 QY 752 GACATACTTCTCGGATCTGGAGCTGCAATTTTACAGAAGCTCGTGACTATTTCT 811
 |||||
 Db 492 GCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTACT 433
 |||||
 QY 812 AATAATGTAAGTTTCCTTTTATTGACAAATAGGTCAAGGAGGAGCTCTTCAACACG 871
 |||||
 Db 432 GCTGCTGCTACTACTACTGCTAACTACTACTACTACTGCTGCTGCTACTACTACT 373
 |||||
 QY 872 GGGGATATGTCAGGAGGTGCTATCTGCTTATTAATAACTAGTACAGATACT 922
 |||||

[illegible]

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CNS014J2      1025 bp      DNA      linear      GSS 26-JUL-1999
LOCUS      Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION      BACN1111 of DrosBAC library from Drosophila melanogaster (fruit
COMMENT      fly), genomic survey sequence.
ACCESSION      AL104216
VERSION      AL104216.1 GI:5615827
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 1025)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBAC11.
FEATURES      Location/Qualifiers
source      1..1025
             /organism="Drosophila melanogaster"
             /mol_type="genomic DNA"
             /db_xref="taxon:7227"
             /clone="BACN1111"
             /clone_lib="DrosBAC"
             /plasmid="pBeloBAC11"
             /note="end : T7"
ORIGIN
Query Match      1.5%; Score 44.4; DB 29; Length 1025;
Best Local Similarity 42.6%; Pred. No. 4.3;
Matches 52; Conservative 29; Mismatches 41; Indels 0; Gaps 0;

QY      27 AATCTCTGACCTGTTCTCCTCGTATCTTAAATATTAATTAATCAAAATCAA 86
Db      600 MACHTTTAMGTTATMTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 659

QY      87 GTATATATTTTACAAATGAAGTCTTCTTCCCAAGTTGTATTTCTACATTTGCTATT 146
Db      660 ATWTATWTWTACATTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 719

QY      147 TC 148
Db      720 YC 721

RESULT 13
BM881804/c
LOCUS      BM881804 450 bp mRNA linear EST 25-APR-2002
DEFINITION      rb14b09.y1 Meloidogyne incognita egg pAMP1 Bird Meloidogyne
incognita cDNA 5', mRNA sequence.
ACCESSION      BM881804
VERSION      BM881804.1 GI:19265548
KEYWORDS      EST.
SOURCE      Meloidogyne incognita (southern root-knot nematode)
ORGANISM      Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE      1 (bases 1 to 450)
AUTHORS      McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarisshvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

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Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCaun, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by David Bird (david.bird@ncsu.edu).
DNA Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco
High quality sequence stop: 402.
FEATURES      Location/Qualifiers
source      1..450
             /organism="Meloidogyne incognita"
             /mol_type="mRNA"
             /db_xref="taxon:6306"
             /dev_stage="egg"
             /lab_host="DH108"
             /clone_lib="Meloidogyne incognita egg pAMP1 Bird"
             /notes="vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was provided by Dr. David Bird at North
Carolina State University, Raleigh, NC
(david.bird@ncsu.edu). The cDNA was made by using Dynabead
oligo-dT priming (Dyna). PCR based library using a
modified protocol from the SMART PCR cDNA Synthesis Kit
from Clontech. Directionally cloned into the UDG sites of
pAMP1."
ORIGIN
Query Match      1.5%; Score 44; DB 12; Length 450;
Best Local Similarity 53.5%; Pred. No. 4.9;
Matches 92; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY      56 TATCTCTTAAATTAATTAATTCAAATCAAGATATATATTTTACATGAAGTCTTCTTTC 115
Db      316 TATTTTGAGCATCTTAACCAAAATATCTACTAAATAATTTACTTAAATCTTCTTCC 257

QY      116 CCCAAGTTTGTAATTTTACATTTGCTATTTTCCCTTTGTCTATGATGTCACGAGACA 175
Db      256 AATATTTTGTTAGTCTCTCCATTTATTTTGTCTTTTATTTTATAGTTCATAAAT 197

QY      176 GTTTTGATTCAGTGGAGTTCGATTCGGATRAAATGTAATTTTTCAG 227
Db      196 TCITTTGAATGTTCAAAATCGTTTGAATCAACAAAAAATGTAATAATTTTAG 145

RESULT 14
BG602722/c
LOCUS      BG602722 498 bp mRNA linear EST 14-AUG-2001
DEFINITION      EST501812 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA
clone PYCDJ76, mRNA sequence.
ACCESSION      BG602722
VERSION      BG602722.1 GI:15152736
KEYWORDS      EST.
SOURCE      Plasmodium yoelii
ORGANISM      Plasmodium yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE      1 (bases 1 to 498)
AUTHORS      Kappe, S.H.I., Gardner, M.J., Brown, S.M., Ross, J., Matuschewski, K.,
Ribeiro, J.M., Adams, J.H., Quackenbush, J., Cho, J., Carucci, D.J.,
Hoffman, S.L. and Nussenzweig, V.
Exploring the transcriptome of the malaria sporozoite stage
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9895-9900 (2001)
21396555
11493695
CONTACT: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA

```

Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org
 Request for clones, please contact: Stefan Kappe,
 kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
 Department of Pathology New York University School of Medicine.

FEATURES

source

Location/Qualifiers
 1. .498
 /organism="Plasmodium yoelii"
 /mol_type="mRNA"
 /strain="17XNL"
 /db_xref="taxon:5861"
 /clone="PYCDJ76"

/dev_stage="sporozoites from salivary gland"
 /lab_host="E. coli TOP10"
 /clone_lib="Plasmodium yoelii sporozoite cDNA"
 /notes="Vector: pCR4; TA cloning; Plasmodium yoelii
 sporozoite cDNA library from salivary gland sporozoites 14
 days post-infection"

ORIGIN

Query Match 1.5%; Score 44; DB 12; Length 498;
 Best Local Similarity 56.1%; Pred. No. 4.9;
 Matches 83; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 15 AGAGGTTGAGTGAATTCCTGACTGCTTTCTCCTATTTGGTGATCTCTTAAATATATAA 74
 |||||
 Db 209 AGTGGTCTATTTTATCTTTGATTTTTTTTAGCTCTCTTACATTTCTTCAAAATATTTT 150
 |||||
 QY 75 TTCAAAATCAAGTATATATTTTACAAATGAAGTCTTTTCCCAAGTTTGATTTTCTTA 134
 |||||
 Db 149 TATCAAAATATACACTTTTTTTTTTTTAAAGTATTTTTTGTCTAATTCGTTTTTCGT 90
 |||||
 QY 135 CATTGCTATTTTCCCTTTGTCTATGAT 162
 |||||
 Db 89 TTATCGTTTCTTATACATTTCTTTCAT 62
 |||||

RESULT 15

BG602721/c

LOCUS

DEFINITION EST501811 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA
 clone PYCDJ76, mRNA sequence.

ACCESSION

BG602721

VERSION

BG602721.1 GI:15152735

KEYWORDS

EST.

SOURCE

Plasmodium yoelii

ORGANISM

Plasmodium yoelii

REFERENCE

AUTHORS

Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,

Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,

Hoffman,S.L. and Nussenzweig,V.

Exploring the transcriptome of the malaria sporozoite stage

Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9895-9900 (2001)

21396555

PUBMED

11493695

COMMENT

Contact: Malcolm J. Gardner

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 3519

Fax: 301 838 0208

Email: gardner@tigr.org

Request for clones, please contact: Stefan Kappe,

kappes01@popmail.med.nyu.edu Michael Heidelberger Division,

Department of Pathology New York University School of Medicine.

FEATURES

source

Location/Qualifiers
 1. .593
 /organism="Plasmodium yoelii"
 /mol_type="mRNA"
 /strain="17XNL"
 /db_xref="taxon:5861"

/clone="PYCDJ76"
 /dev_stage="sporozoites from salivary gland"
 /lab_host="E. coli TOP10"
 /clone_lib="Plasmodium yoelii sporozoite cDNA"
 /notes="Vector: pCR4; TA cloning; Plasmodium yoelii
 sporozoite cDNA library from salivary gland sporozoites 14
 days post-infection"

ORIGIN

Query Match 1.5%; Score 44; DB 12; Length 593;
 Best Local Similarity 56.1%; Pred. No. 5;
 Matches 83; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 15 AGAGGTTGAGTGAATTCCTGACTGCTTTCTCCTATTTGGTGATCTCTTAAATATATAA 74
 |||||
 Db 209 AGTGGTCTATTTTATCTTTGATTTTTTTTAGCTCTCTTACATTTCTTCAAAATATTTT 150
 |||||
 QY 75 TTCAAAATCAAGTATATATTTTACAAATGAAGTCTTTTCCCAAGTTTGATTTTCTTA 134
 |||||
 Db 149 TATCAAAATATACACTTTTTTTTTTTTAAAGTATTTTTTGTCTAATTCGTTTTTCGT 90
 |||||
 QY 135 CATTGCTATTTTCCCTTTGTCTATGAT 162
 |||||
 Db 89 TTATCGTTTCTTATACATTTCTTTCAT 62
 |||||

Search completed: August 16, 2004, 18:43:21
 Job time : 4920 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 07:10:13 ; Search time 7610 Seconds
(without alignments)
17086.610 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 3000
Sequence: 1 cgccttaactagtagaggt.....tgctttgctaaacactttc 3000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
6940544

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_hg_hum.*
- 31: em_hg_inv.*
- 32: em_hg_other.*
- 33: em_hg_mus.*
- 34: em_hg_pln.*
- 35: em_hg_rod.*
- 36: em_hg_mam.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_higo_hum.*
- 40: em_higo_mus.*
- 41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3000	100.0	3000	6	BD261378	Chlamydia
2	2988	99.6	16448	1	AE001587	AE001587 Chlamydia
3	2988	99.6	26920	1	CPN133035	AJ133035 Chlamydia
4	2986.4	99.5	12127	1	AE002235	AE002235 Chlamydia
5	2986.4	99.5	239650	1	AP002545	AP002545 Chlamydia
6	2984.8	99.5	300923	1	AE017157	AE017157 Chlamydia
7	2975.4	99.2	110000	6	AR310754_00	AR310754 Sequence
8	2775.8	92.5	2787	6	A81835	A81835 Sequence 9
9	2775.8	92.5	2787	6	BD192261	BD192261 Surface e
10	2241	74.7	2241	6	AX349497	AX349497 Sequence
11	570.4	19.0	300512	1	AE016995	AE016995 Chlamydia
12	546.6	18.2	2781	6	AX662119	AX662119 Sequence
13	546.6	18.2	2781	6	AX666191	AX666191 Sequence
14	546.6	18.2	4926	1	CPU72499	U72499 Chlamydophi
15	533.2	17.8	300380	1	AE017158	AE017158 Chlamydia
16	531.8	17.7	12676	1	AE002192	AE002192 Chlamydia
17	531.8	17.7	300650	1	AP002546	AP002546 Chlamydia
18	531.2	17.7	10757	1	AE001628	AE001628 Chlamydia
19	530.2	17.7	2815	6	A81829	A81829 Sequence 3
20	530.2	17.7	2815	6	BD192258	BD192258 Surface e
21	530.2	17.7	17280	1	CPN133034	AJ133034 Chlamydia
22	527	17.6	2787	6	AX349573	AX349573 Sequence
23	524.6	17.5	2957	6	BD244667	BD244667 Chlamydia
24	523	17.4	534	6	AX349495	AX349495 Sequence
25	522.2	17.4	2757	6	A81837	A81837 Sequence 11
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33	516.6	17.2	10757	1	AE001628	AE001628 Chlamydia
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35	515.2	17.2	2784	6	BD261386	BD261386 Chlamydia
36	515.2	17.2	15068	1	AE001627	AE001627 Chlamydia
37	515	17.2	2787	6	A81839	A81839 Sequence 13
38	515	17.2	2787	6	BD192263	BD192263 Surface e
39	515	17.2	12676	1	AE002192	AE002192 Chlamydia
40	514	17.1	2793	6	A81841	A81841 Sequence 15
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44	512.6	17.1	2950	6	BD261383	BD261383 Chlamydia
45	509.8	17.0	110000	6	AR310754_05	Continuation (6 of

ALIGNMENTS

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DEFINITION	thereof					
ACCESSION	BD261378					
VERSION	BD261378.1	GI:33071146				
KEYWORDS	JP 2002528111-A/1.					
SOURCE	Chlamydophila pneumoniae					
ORGANISM	Chlamydophila pneumoniae					
REFERENCE	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.					
AUTHORS	1 (bases 1 to 3000)					
TITLE	Murdin,A.D., Oomen,R.P. and Dunn,P.L.					
JOURNAL	Chlamydia antigens and corresponding DNA fragments and uses thereof					
	Patent: JP 2002528111-A 1 03-SEP-2002;					

CONNAUGHT LABORATORIES LTD	
OS	Chlamydia pneumoniae
PN	JP 2002528111-A/1
PD	03-SEP-2002
PF	29-OCT-1999 JP 2000579624
PR	29-OCT-1998 US 60/106070,01-MAR-1999 US 60/122066 PR
PI	ANDREW DAVID MURDIN, RAYMOND PETER OOMEN, PAMELA LESLEY DUNN PC
C12N15/09, A61K35/74, A61K35/76, A61K39/118, A61K39/385, A61K39/39, PC	
A61K48/00,	
PC A61P31/00, C07K14/295, C07K16/12, C07K19/00, C12N1/15, C12N1/19, PC	
C12N1/21,	
PC C12N5/10, C12P21/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/566, PC	
G01N33/569,	
PC G01N33/577//C12P21/08, C12N15/00, C12N5/00	
CC Chlamydia antigens and corresponding DNA fragments and uses	
CC thereof	
PH Key	Location/Qualifiers
FT CDS	(101)..(2884).
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Best Local Similarity 100.0%; Pred. No. 0;	
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB 1	CGCTCTTACCTAGTAGAGTTGAGTGAATTTCTTGACTTCTTTCTCTCTATTTGGTATCT 60
QY 61	CTTAAATATTAATCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCAA 120
DB 61	CTTAAATATTAATCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCAA 120
QY 121	GTTTGTATTTTACATTTTGTCTATTTTCCCTTTTGTCTATGATTTGCTACCGAGACAGTTT 180
DB 121	GTTTGTATTTTACATTTTGTCTATTTTCCCTTTTGTCTATGATTTGCTACCGAGACAGTTT 180
QY 181	GGATTCAAGTGCAGTTTCGATGGGAATAAATGGTAAATTTTTCAGTTTCTGTCAGAGTCA 240
DB 181	GGATTCAAGTGCAGTTTCGATGGGAATAAATGGTAAATTTTTCAGTTTCTGTCAGAGTCA 240
QY 241	GGAGATGCTGGAACTACCTACTATTTAAGGGAATGTCACTCTAGAAAATTTCTCTGG 300
DB 241	GGAGATGCTGGAACTACCTACTATTTAAGGGAATGTCACTCTAGAAAATTTCTCTGG 300
QY 301	AACAGGCACAGCAATCACAAAAGCTTTTAAACAACACTAAGGGGATTTGACTTTTAC 360
DB 301	AACAGGCACAGCAATCACAAAAGCTTTTAAACAACACTAAGGGGATTTGACTTTTAC 360
QY 361	AGGTAAACGGAACTCTCTATTGTTCAAAACGGTGGATGAGGAGTGTAGCAGGGGCTGC 420
DB 361	AGGTAAACGGAACTCTCTATTGTTCAAAACGGTGGATGAGGAGTGTAGCAGGGGCTGC 420
QY 421	TGTTAAACAGCAGCGTGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGCTATCTTT 480
DB 421	TGTTAAACAGCAGCGTGTAGATAAATCTACACAGTTTATAGGGTTTCTTCGCTATCTTT 480
QY 481	TATTTCGCTCTCTGGAAGTTCCATTAACCTACCGCAAGAGCGGTAGTGTCTACGGG 540
DB 481	TATTTCGCTCTCTGGAAGTTCCATTAACCTACCGCAAGAGCGGTAGTGTCTACGGG 540
QY 541	TAGCTTGAGTTTGACAAAATATGTCAGTTTGTCTTTTACGAAAATCTTTTCAACGGATAA 600
DB 541	TAGCTTGAGTTTGACAAAATATGTCAGTTTGTCTTTTACGAAAATCTTTTCAACGGATAA 600
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DB 601	TGCGCGTGTATCACCGGAAAATCTTTTCATTAACAGGACTACAAATGTCAGCTCTGTT 660
QY 661	TTCTGAAAATACCTCTCTCAAAAGAGCGGAGCATTTCAGACTTCCGATGCCCTTACCAT 720
DB 661	TTCTGAAAATACCTCTCTCAAAAGAGCGGAGCATTTCAGACTTCCGATGCCCTTACCAT 720
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DB 721	TACTGGAAACCAAGGGGAAGTCTCTTTTCTGACAAATCTTCTTCGATTTCTGGAGCTGC 780
QY 781	AAATTTTACAGAGCCTCGGTGACTATTTCTTAATGCTAAAGTTTCTTTTATGACAA 840
DB 781	AAATTTTACAGAGCCTCGGTGACTATTTCTTAATGCTAAAGTTTCTTTTATGACAA 840
QY 841	TAAGGTCACAGGAGCCTCTCAACAAACGGGGGATATGTCAGAGGCTGCTATCTGTC 900
DB 841	TAAGGTCACAGGAGCCTCTCAACAAACGGGGGATATGTCAGAGGCTGCTATCTGTC 900
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DB 901	TTATAAATCTAGTACAGATCTAAGGTCAACCTCACTGGAAATCAGATGTTACTTTCAG 960
QY 961	CAACAATACATCGACAACACGGGAGAGCTATCTATGTGAAAAGCTCGAATGGCTTC 1020
DB 961	CAACAATACATCGACAACACGGGAGAGCTATCTATGTGAAAAGCTCGAATGGCTTC 1020
QY 1021	CGGAGGACTTACCTCTATTTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTTAAAGTGG 1080
DB 1021	CGGAGGACTTACCTCTATTTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTTAAAGTGG 1080
QY 1081	AGCCATAGCTATCGAAGTAGTGGGAAATGAGTTTATCCGCCGATAGTGGTGAATTTG 1140
DB 1081	AGCCATAGCTATCGAAGTAGTGGGAAATGAGTTTATCCGCCGATAGTGGTGAATTTG 1140
QY 1141	CTTTTATAGGAAATACAGTCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
DB 1141	CTTTTATAGGAAATACAGTCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
QY 1201	AGGAACGAGTGCAGGATGACAGCTTTGGGTTCTGCTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1201	AGGAACGAGTGCAGGATGACAGCTTTGGGTTCTGCTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261	TGATCCCAATACCTACAGGATCATCAACAGTTACAGATGTCTTAAAGTTTAAATGAGAC 1320
DB 1261	TGATCCCAATACCTACAGGATCATCAACAGTTACAGATGTCTTAAAGTTTAAATGAGAC 1320
QY 1321	TCCGGCAGATTTCTGCACTACATATACAGGAACTATCTTCAAGGAGGAAAGTTATC 1380
DB 1321	TCCGGCAGATTTCTGCACTACATATACAGGAACTATCTTCAAGGAGGAAAGTTATC 1380
QY 1381	AGAGACAGAGGCGCGAGATTTTAAATCTTCTTGAAGTCTACAGCTGTAACTCT 1440
DB 1381	AGAGACAGAGGCGCGAGATTTTAAATCTTCTTGAAGTCTACAGCTGTAACTCT 1440
QY 1441	TTTCAAGGAGTCTCTATCTTTTAAACATGAGGAGTCTGCGAGCTCAGGCAATCTCA 1500
DB 1441	TTTCAAGGAGTCTCTATCTTTTAAACATGAGGAGTCTGCGAGCTCAGGCAATCTCA 1500
QY 1501	ACAGGCAGATTTCTGCTCGAAATGGAGTGTAGAACTACTCTAGAACCTGCTGATACTAG 1560
DB 1501	ACAGGCAGATTTCTGCTCGAAATGGAGTGTAGAACTACTCTAGAACCTGCTGATACTAG 1560
QY 1561	CACCATAAACAAATTTGGTCAATTAACATCAGTTTCTATAGACGGTCAAGAGGCAAAAT 1620
DB 1561	CACCATAAACAAATTTGGTCAATTAACATCAGTTTCTATAGACGGTCAAGAGGCAAAAT 1620
QY 1621	AGAAACCAAGCTACGTAAGAAATCTGACTTTTATCTGGAACCATCTTTTATGAGCC 1680
DB 1621	AGAAACCAAGCTACGTAAGAAATCTGACTTTTATCTGGAACCATCTTTTATGAGCC 1680
QY 1681	GACGGGACGTTTATGAAAATCATAGTTTAAAGAAATCTCTAGTCTCTACGATCTTAGA 1740
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QY	1801	GAATTTCCATTACGGCTATCAGGGAATCTGGGCCCAATTTGTTGGGGACAGGGGCTTC	1860
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QY	1861	TAGGACTGCAACCTTCAACTGGAATAAACTGCTATATTCCTAAATCCCGAGGATTCGG	1920
Db	1861	TAGGACTGCAACCTTCAACTGGAATAAACTGCTATATTCCTAAATCCCGAGGATTCGG	1920
QY	1921	CTCTTTAGTCCCTAATAGCTATATGGATGCAATTTATAGTATATAGCTCTCTCCATTATCT	1980
Db	1921	CTCTTTAGTCCCTAATAGCTATATGGATGCAATTTATAGTATATAGCTCTCTCCATTATCT	1980
QY	1981	TATGGAGCTGCAACCAAGGGTTGACGGAGACCGTGCTTTTGGTGTGCTCGATTATC	2040
Db	1981	TATGGAGCTGCAACCAAGGGTTGACGGAGACCGTGCTTTTGGTGTGCTCGATTATC	2040
QY	2041	TAACTTCTTCCATAAGGATAGTACAAAAACACGACGGGGTTTCGCCATTGAGTGGCGG	2100
Db	2041	TAACTTCTTCCATAAGGATAGTACAAAAACACGACGGGGTTTCGCCATTGAGTGGCGG	2100
QY	2101	TTATGTCATAGGAGGAACCTACATACCTTGTTCAGATAAGATTCCTTAGTGTGCAATTTG	2160
Db	2101	TTATGTCATAGGAGGAACCTACATACCTTGTTCAGATAAGATTCCTTAGTGTGCAATTTG	2160
QY	2161	TCAGCTCTTTGGAGAGATAGACTACTTTGTAGCTAAGAAATCAAGTACAGTCTACGG	2220
Db	2161	TCAGCTCTTTGGAGAGATAGACTACTTTGTAGCTAAGAAATCAAGTACAGTCTACGG	2220
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Db	2281	TTGTTGCTGTTTATGTTCTCAGAGATTCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCT	2340
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Db	2581	TCTTCCCTTACTATCGGATCCGATTTGATAGAAATCAGACTGCGCAAGATGCAACGTA	2640
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Db	2941	ATTTCTTGAAGGCTCTTTTCGATTTCCGATTTCCATTTTAGTGTCTTAAACACTTTC	3000

RESULT 2

AE001587

LOCUS

Chlamydia pneumoniae section 3 of 103 of the complete genome.

DEFINITION

AE001587 AE001587

ACCESSION

AE001587.1 GI:4376271

VERSION

1 (bases 1 to 16448)

KEYWORDS

Chlamydia pneumoniae CWL029

SOURCE

Chlamydia pneumoniae CWL029

ORGANISM

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE

1 (bases 1 to 16448)

AUTHORS

Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.

TITLE

Comparative genomes of Chlamydia pneumoniae and C. trachomatis

JOURNAL

Nat. Genet. 21 (4), 385-389 (1999)

MEDLINE

9206606

PUBMED

1019388

REFERENCE

2 (bases 1 to 16448)

AUTHORS

Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.

TITLE

Direct Submission

JOURNAL

Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA

FEATURES

source

1. 16448

Location/Qualifiers

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 hb1, hb2, hb3, hb4, hb5, hb6, hb7, omp7, pseudogenes omp8, omp9,
 omp15, strain VR1310.
 ACCESSION AJ133035
 VERSION AJ133035.1 GI:4455890
 KEYWORDS hb1 gene; HB2 gene; hb3 gene; hb4 gene; hb5 gene; hb6 gene; hb7
 gene; omp15 gene; omp6 gene; omp7 gene; omp8 gene; omp9 gene; outer
 membrane protein 6; outer membrane protein 7; pseudogene.
 SOURCE Chlamydia pneumoniae
 ORGANISM Chlamydia pneumoniae
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
 1
 Daugaard, L., Hjertoen, K., Knudsen, K., Madsen, A. S., Christiansen, G.
 and Birkelund, S.
 Unpublished
 2 (bases 1 to 26920)
 Boesen, T.
 Direct Submission
 Submitted (21-JAN-1999) Boesen T., Department of Medical
 Microbiology and Immunology, University of Aarhus, The Bartholin
 Building, DK-8000 Aarhus, DENMARK
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VERSION	AE002235.2	GI:8163495	
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SOURCE	Chlamydia pneumoniae AR39		
ORGANISM	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia		
REFERENCE	1 (bases 1 to 12127)		
AUTHORS	Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.		
TITLE	Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39		
JOURNAL	Nucleic Acids Res. 28 (6), 1397-1406 (2000)		
MEDLINE	20150255		
PUBMED	10684935		
REFERENCE	2 (bases 1 to 12127)		
AUTHORS	Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.		

Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT
On Jun 1, 2000 this sequence version replaced gi:7189672.
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1 Shirai, M., Hirakawa, H., Ouchi, K., Tabuchi, M., Kishi, F., Kimoto, M.,
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genome sequences of Chlamydia pneumoniae isolates from Japan and
the United States
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2 Shirai, M., Hirakawa, H., Kimoto, M., Tabuchi, M., Kishi, F., Ouchi, K.,
Shiba, T., Ishii, K., Hattori, M., Kuhara, S. and Nakazawa, T.
Comparison of whole genome sequences of Chlamydia pneumoniae J138
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Nucleic Acids Res. 28 (12), 2311-2314 (2000)
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Shirai, M.
Direct Submission
Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University
School of Medicine, Department of Microbiology; 1-1-1
Minamikogushi, Ube, Yamaguchi 755-8505, Japan
(E-mail: mshirai@po.cc.yamaguchi-u.ac.jp, Tel: 81-836-22-2227,
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VERSION AE017157.1 GI:33235843
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AUTHORS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomphila.
Geng,M.M., Schuhmacher,A., Muehldorfer,I., Bensch,K.W.,
Schaefer,K.P., Schneider,S., Pohl,T., Essig,A., Marre,R. and
Melchers,K.
The genome sequence of Chlamydia pneumoniae TW183 and comparison
with other Chlamydia strains based on whole genome sequence
analysis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 300923)
AUTHORS Geng,M.M., Schuhmacher,A., Muehldorfer,I., Bensch,K.W.,
Schaefer,K.P., Schneider,S., Pohl,T. and Melchers,K.
Direct Submission
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JOURNAL Byk-Gulden-Str. 2, Konstanz 78467, Germany
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VERSION A81835.1 GI:6731868			
KEYWORDS .			
SOURCE unidentified			
ORGANISM unidentified			
REFERENCE 1 (bases 1 to 2787)			
AUTHORS Madsen,A. and Birkelund,S.			
TITLE NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE			
JOURNAL Patent: WO 9858953-A 9 30-DEC-1998;			
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ACCESSION BD192261
VERSION BD192261.1 GI:33002000
KEYWORDS JP 2002510970-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2787)
AUTHORS Birkelund,S., Christensen,G., Knudsen,K., Madsen,A.S. and
Mygind,P.
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JOURNAL Patent: JP 2002510970-A 5 09-APR-2002;
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DEFINITION Chlamydomophila caviae GPIC section 2 of 4 of the complete genome.
ACCESSION AE016995 AE015925
VERSION AE016995.1 GI:29834389
KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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JOURNAL

FEATURES

source

Chlamydomophila caviae GPIC
Chlamydomophila caviae GPIC
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
1 (bases 1 to 300512)
Read, T.D., Myers, G.S., Brunham, R.C., Nelson, W.C., Paulsen, I.T.,
Heidelberg, J., Holtzapple, E., Khouri, H., Fedorova, N.B., Carty, H.A.,
Umayam, L.A., Haft, D.H., Peterson, J., Beanan, M.J., White, O.,
Saizberg, S.L., Hsia, R.C., McClarty, G., Rank, R.G., Bavoi, P.M. and
Fraser, C.M.
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examining the role of niche-specific genes in the evolution of the
Chlamydiaceae
Nucleic Acids Res. 31 (8), 2134-2147 (2003)
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2 (bases 1 to 300512)
Read, T., Myers, G., Brunham, R., Nelson, W., Paulsen, I.,
Heidelberg, J., Holtzapple, E., Khouri, H., Fedorova, N., Carty, H.,
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LOCUS AX666191 2781 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 56 from Patent WO0247718.
ACCESSION AX666191
VERSION AX666191.1 GI:29290994
KEYWORDS Chlamydomophila psittaci
SOURCE Chlamydomophila psittaci
ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
REFERENCE 1
AUTHORS Johnston, S.A.
TITLE Methods and compositions for vaccination comprising nucleic acid
JOURNAL ad/or polypeptide sequences of i(chlamydia)
PATENT Patent: WO 0247718-A 56 20-JUN-2002;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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RESULT 14					
CPU72499					
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DEFINITION	Chlamydoiphila abortus putative outer membrane protein gene, partial cds; and putative 98 kDa outer membrane protein gene, complete cds.				
ACCESSION	U72499				
VERSION	U72499.1	GI:1657776			
KEYWORDS	Chlamydoiphila abortus				
SOURCE	Chlamydoiphila abortus				
ORGANISM	Bacteria; Chlamydiaceae; Chlamydiales; Chlamydoiphila.				
REFERENCE	1 (bases 1 to 4926)				
AUTHORS	Longbottom,D., Russell,M., Dunbar,S.M., Jones,G.E. and Herring,A.J.				
TITLE	98kDa protein genes from ovine abortion strain S26/3 Chlamydia				

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Job time : 7625 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	140.6	4.7	3354	4	US-09-612-402B-23
5	133.8	4.5	3324	4	US-09-612-402B-24
6	132.2	4.4	3021	4	US-09-556-877-182
7	132.2	4.4	3021	4	US-09-620-412C-182
8	132.2	4.4	3021	4	US-09-598-419-182
9	132.2	4.4	4435	4	US-09-612-402B-1
10	131.4	4.4	2949	4	US-09-556-877-170
11	131.4	4.4	2949	4	US-09-620-412C-170
12	131.4	4.4	2949	4	US-09-598-419-170
13	130.6	4.4	1444	4	US-09-612-402B-11
14	61.2	2.0	3050	4	US-09-427-533B-1
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19	50.4	1.7	1515	4	US-09-612-402B-22
20	50.2	1.7	2601	4	US-09-556-877-181
21	50.2	1.7	2601	4	US-09-620-412C-181
22	50.2	1.7	2601	4	US-09-598-419-181
23	42.6	1.4	832	4	US-09-621-976-2813
24	42.4	1.4	474	4	US-09-621-976-18033
25	42.4	1.4	6124	4	US-08-213-419B-3
26	39.6	1.3	580073	4	US-08-545-528D-1
27	39	1.3	1896	4	US-09-620-412C-324

28	39	1.3	1896	4	US-09-598-419-324	Sequence 324, App
29	37.6	1.3	1965	4	US-09-620-412C-340	Sequence 340, App
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31	37.6	1.3	2076	4	US-09-620-412C-312	Sequence 312, App
32	37.6	1.3	2076	4	US-09-598-419-312	Sequence 312, App
33	37.6	1.3	5265	4	US-09-556-877-174	Sequence 174, App
34	37.6	1.3	5265	4	US-09-620-412C-174	Sequence 174, App
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36	36.8	1.2	1269	2	US-08-758-621-11	Sequence 11, Appl
37	36.8	1.2	1269	3	US-09-107-858-11	Sequence 11, Appl
38	36.8	1.2	1269	4	US-09-579-174-11	Sequence 94, Appl
39	36.8	1.2	1497	4	US-09-220-132-94	Sequence 184, App
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43	36	1.2	2895	4	US-09-556-877-171	Sequence 171, App
44	36	1.2	2895	4	US-09-620-412C-171	Sequence 171, App
45	36	1.2	2895	4	US-09-598-419-171	Sequence 171, App

ALIGNMENTS

RESULT 1

US-09-198-452A-1

; Sequence 1, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1

; LENGTH: 1230025

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

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Matches 2998; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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DB 31898 GGAAGATGCTGGAATCTACCTACCTATTTTAAGGGAATGTCACCTAGAGAAATATTCTGTG 31957
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RESULT 2

US-09-198-452A-1/c

; Sequence 1, Application US/09198452A

; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198.452A
; CURRENT FILING DATE: 1998-11-24
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Query Match 17.0%; Score 509.8; DB 4; Length 1230025;

Best Local Similarity 52.7%; Pred. No. 2.2e-142;

Matches 1410; Conservative 0; Mismatches 1184; Indels 81; Gaps 11;

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Qy 307 CACAGCAATCAGAAAAGCTGTTTAAACACACTAAGGGGATTTGACITTCACAGGTAA 366
Db 517986 --CAGCTTTAACGAAGGGTTGTTTTCTGACACTACGGAATCTTTAAGCTTTTCCCGGTAA 517929

Qy 367 CGGGAACCTCTATTGTTTCCAAACGGTGGATGACGAGACTGTAGAGGGGCTGCTGTAA 426
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Qy 427 CAGCAGCGTGTAGATAAAATCTACCAAGTTTATAGGGTTTTCTTCGCTATCTTTTATTGC 486
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QY	487	GTCTCTCGAAGTTCGATAAATACCGGCAAAAGGCGGTAGCT---GCTCTACGGGTAG	543	QY	1547	CC---TGCTGATPACTAGACCAATAAACAATTTGGTCATTTAAACATCAGTTCTTATAGACGGT	1603
Db	517815	GGCCCCATCATCGGTAAATACAAACCCCTCAGAAAGGTGCAGTTAAATGTGGAGGGA	517756	Db	516768	GCAAGTCACAGAGGAGGTCACTTTAAACAGGTCTTTCCATCTCTGTAGACTCTTTAGCGGAG	516709
QY	544	CTTGAGTTTGACAAAAATGTGAGTTTGTCTTTCAGCAAAAACTTTTCAACGGATAATGG	603	QY	1604	GCAAAAGGCGAAATAAGAACCAACCAAGCTACGTCAAAAATCTGACTTTATCTGGAACC	1663
Db	517755	TCTTACATTTGTATAACAATGGAACATATTTTATTTAAACAAGATTACTGTGAGAAAAATGG	517696	Db	516708	GGTAAAGATTGTAATTTGCTGCTTCTGACGAAAGTAATAATGTAGCCCTTGTAGTCTCG	516649
QY	604	CGGTCTATCAGCGCAAAACCTTTTCTATACAGGGACTCAATGTGAGCTCTGTTTC	663	QY	1664	ATCACCTTTATTGGAACCCGACGGGACGTTTATGAAAATCATAGTTTAAAGAAATCCTCAG	1723
Db	517695	CGGACATTTCTACCAAGATCTTTCTTTGAAAAACAGACGGGATCGATTTCTTTTGAAG	517636	Db	516648	ATTCTTCTTTTGGATTAACCAAGGGATGCTTATGAATACACGACTTAGNAAAATCTCAA	516589
QY	664	TGAAAAATA-----CCTCTCAAAAGAAAGGCGGACCATTCAGACTTCCGATGCCCTTA	716	QY	1724	TCTTACGACATCTTAGAGCTCAAGCTTCTTGAACTGTGAACTGTAAACGACCGCAGTGCAC	1783
Db	517635	GGAAATAATCGAGCGCAACAGGGAATAAGGTGGGCTATTTGTGCTACTGTGACTGTAG	517576	Db	516588	GACTTTTCAATTTGTGAGCTCTCTGCTCTGGTACTGCAACAACATACAGATGTTCCAGCG	516529
QY	717	CAATTAATGGAACCAAGGGGAAGTCTCTTTTCTGCAAAATCTTCTTCGGAATTCGGAG	776	QY	1784	GATCTATAATGGGTGAGAAATTCATTACGGCTATCAGGAACTTGGGGCCCAATTGTT	1843
Db	517575	ATATTACAAATAATACGGCTCCTCAACCAACGGGGATATGTCAGGAGTGCAGGTG	517516	Db	516528	GTTCCTACAGTAGCAACTCTTACGCACATATGGGTATCAAGGTACTTGGGGAATGACTGG	516469
QY	777	CTGCAATTTTACAGAAGCTCGGTGACTATTTCTAAATAATGCTAAAGTTTCTCTTTATTG	836	QY	1844	TGGG-----GGACAGGGGCTTCTAGACTGCAACCTTCAACTTGGACTTAAACT	1891
Db	517515	GAGCTATAAATAGCAGGAACCTGTACAAATACAGGGGAATACGTCCTTGTATTTCTG	517456	Db	516468	GTTGATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACG	516409
QY	837	ACAATAAGGTACAGAGCGAGCTCCTCAACAACGGGGATATGTCAGGAGGTGCTATCT	896	QY	1892	GGCTATATTCTTAATCCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCA	1951
Db	517455	AAAATAGTGTGAC---AGCGACCGAGGAATGGAGGAGCTCTTTCTGG-----	517410	Db	516408	GGCTACCTTCCGAATCTGAGCGTCAAGGACCTTTAGTTCTCTTAATAGCCTTTGGGATCT	516349
QY	897	GTGCTTTAATAACTAGTACAGATCTAAGGTCACTGCACTCTCTGCAATCAGATGTTACTCT	956	QY	1952	TTTATAGATATTAGCTCTCTCCATATCTTATGGAGACTGCAACGAGGGTTGCAGGGA	2011
Db	517409	-----AGATGCGGATGTTTACCATATCTGGGAATCAGAGTGAACCT	517369	Db	516348	TTTTCAGACATCCAAGCAATCCAAGGTGTCATAGAGAGAGTGTCTTTGACTCTTTGTTCA	516289
QY	957	TCAGCAACAATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTCG	1016	QY	2012	GACCGTGTCTTTTGGTGTGCTCGATTTATCTAACTTCTTCCATAAGGATAGTACAAAAACA	2071
Db	517368	TCTCAGAAACCAACGTGTAGCTAATGCGCGAGCCATTTATGCTAAGAAGCTTACACTGG	517309	Db	516288	GATCAGAGCTCTTGGGCTCGGGAGTCCGCAATTTCTTAGATAAAGATAAGAAAGGGAA	516229
QY	1017	CTTCGGGAGGA-----CTTACCCTATTCACTAGAAATAGTGTCAATGGAGGTACAGCT	1069	QY	2072	CGACGGGGTTTGGCATTGAGTGGCGGTATGTCATAGGAGGAAACCTACATCTTGT	2131
Db	517308	CTTCGGGGGGGGGGGGTATCTCTTTTCTAAATATAGTCCAAGGTACCACCTGCA	517249	Db	516228	AAACCAAAATACCGTCATAAAATCTGGTGATATGCTATCGGAGGTGACGCGCAAACTGT	516169
QY	1070	CCTAAAGGTGGACCATAGCTATCGHAGATAGTGGGGAATAGATTTTATCCGCGGATGT	1129	QY	2132	TCAGATAGATTTCTAGTGTCTGCTCATTTTGTAGCTCTTTTGGAGAGATAGAGACTACTTT	2191
Db	517248	GGTAATGTTGGAGCCATTTCTATCTGCGAGCTGGAGAGTGTAGTCTTTTTCAGCAGAACA	517189	Db	516168	CTGAAACCTTAATTAGCTTTGCTTTTGCCTTTTGCCTTTTGGAGCGATTAAGATTTCTTTA	516109
QY	1130	GGTGACATTTGCTTTTGGGAATACAGTCACTTCTACTACTCC---TGEGACGAATAGA	1186	QY	2192	GTAGCTTAAGAAATCAAGGTACAGTCTACGGAGGAATCTCTATTATCCAGCAACAACGAACC	2251
Db	517188	GGGACATTTACCTTCAATGGGAATGCCATTGTTGCNACTACCAACAACACTACGAAGA	517129	Db	516108	GTGCTAAAAATCATACTGATACCTATGACAGAGCGCTTCTATATCCACACATACAGAA	516049
QY	1187	AGTAGTATCGACTTAGGAACGAGTGCAAGATGACAGCTTTTGGTTCTGCTGCTGTAGA	1246	QY	2252	TATATCTCTCTTCTTGGAACTACGGCCTTGTGCTGTCTTATGTTCTTATGTTCTTACAGAGAT	2311
Db	517128	AATTTCTATTGACATAGGATCTACTGCAAGATCACGAAATTTAGTGTCAATATCTGGGCAT	517069	Db	516048	TGTAGTGGGTTTCATAGTTTGTCTCTTAGATAAA---CTTCTCTGGCTTTGGAGTCAATAA	515992
QY	1247	GCCATCTCTTATGATCCCATACTACAGATCATCCACACAGTTACAGATGCTTTA	1306	QY	2312	CGTGTCTCTTTTCAGGAACCTTAGCTACACCCATACGATAACGATCGAAACCAAG	2371
Db	517068	AGCATCTTTTCTACGATCCGATTTACTGTCTAATACGGCTTCCGGAATCTACAGATACTTTA	517009	Db	515991	CCCTCGTTTTCAGAGGGGAGCTCGCTTATAGCCAGCTCAGTAATGATCTGAAGACAAAG	515932
QY	1307	AAAAGTTAATGAGACTCCGCGAGATCTGCACTACAATATACAGGGAACATCACTTTACA	1366	QY	2372	TATACAACTATCTTACTGTTTAAAGGAAGCTGGGGAATGATAGTTTTCGCTTTTGAATTC	2431
Db	517008	AATCTCAATAAGGTGATCGAGTATAGTACAGATTATAGTGGGTGCAATGTTTCTTCT	516949	Db	515931	TATACTCGGTATCTCGAGGTGAAGGTTCTTGGGGGAAATAATGCTTTTAAATGATGTTG	515872
QY	1367	GGAGAAAGTTATPAGAGACAGGCGCGAGATCTTAAATAATCTTACTTTCGAAGCTACTA	1426	QY	2432	GGTGGAGAGCTCCGATTTGCTTAGATGAAGTGTCTATTTTGGAGAGTACATGCCCCCTTC	2491
Db	516948	GGTGAAGAGCTCTCTGAAGATGAAGCAAAAGTTGACAGCAACCTCTACTTCTACGCTGAAG	516889	Db	515871	GGAGCTTCTTCTCTTCTTATCTCTGAAATACCTGCAATGTTGTTGATACCTATGCTCCATAC	515812
QY	1427	CAGCTGTACTCTTTTCAGGAGTACTCTATCTTTTAAACATGAGTGTGCTCGAGACT	1486	QY	2492	ATGAAATTCAGCTTTGTCTATGCAATCAGGAAGGTTTAAAGAAACAGGGAACAGAGCT	2551
Db	516888	CAGCTGTACTCTAATCGAGGAATTTAGTACTTTAAACGTTGCTGCTACTCTCGATACG	516829	Db	515811	ATCAAACTGAACTGACCTATATATCGTCAGGACAGCTTCTCGGAGAAAGGTACAGAGGA	515752
QY	1487	CAGGCAATTCACCAACAGGAGATCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAA	1546	QY	2552	CGTGAATTTGGAAGTAGCGGTCTTGTGAATCTTGGCTTACCTTATCGGGATCCGATTTGAT	2611
Db	516828	AAAGGCTTTTACTCAGACCGGGGTTCTCTGTGTTATTATGATGCGGGGCAACAGTTAAAA	516769	Db	515751	AGATCTTTTGTAGACAGCAACCTCTTCAATTTTATCTTTGCCTATAGGGGTGAAGTTTGA	515692
				QY	2612	AAGGAATCAGACTGCCCAAGATGCAACGTACAATCTAACTCTTGGTTATATCTGTGGATCTT	2671

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Db 515691 AAGTTCTCTGATTGTAATGACTTTTCTTATGATCTGACTTTATCCTATGTTTCTGTAATCTT 515632
Qy 2672 GTTCGTAGTAACCCGACTGTACGACAACTGCGAATAGCGGTGATTTCTTGAAAACC 2731
Db 515631 ATCCGCAATGATCCCAATGACTACAGCACTTGTATATCAGCGAGGCTCTTTGGGAAACT 515572
Qy 2732 TTCGGTACGAATTTGGCAAGACAGCTTTAGTCTCTGTCGAGGGAACCAATTTTGTCTTT 2791
Db 515571 TATCCCAATTAATAGCAGACAGGCTTGCAGTGGTGAGGCACTACTAGCCCTTC 515512
Qy 2792 AACTCAAAATTTGAAGCCTTTAGCCAAATTTCTTTTGAATTTGCGTGGGTGATCTTCGCAAT 2851
Db 515511 TCTCCTATGTTGAAGTCTCGGCCAGTTTGTCTTTTGAAGTTCGTGGATCTCAGCGATT 515452
Qy 2852 TACAATGTAGACTAGGAGCAAAATACCAATTTCTA 2886
Db 515451 TATAATGTAGACTCTTGGGGGTAAGTTCCAATTTCTA 515417

RESULT 3
US-09-430-723-1
; Sequence 1, Application US/09430723
; Patent No. 6607730
; GENERAL INFORMATION:
; APPLICANT: Murdin, Andrew
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-011
; CURRENT APPLICATION NUMBER: US/09/430,723
; EARLIER FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: 60/106,590
; EARLIER FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/133,071
; EARLIER FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(3019)
US-09-430-723-1

Query Match 8.1%; Score 243.4; DB 4; Length 3150;
Best Local Similarity 49.7%; Pred. No. 3.6e-63;
Matches 1002; Conservative 0; Mismatches 911; Indels 102; Gaps 11;

Qy 914 ACAGATACTAAGGTCAACCTCTCACTGGAAATCAGATGTTACTCTTTCAGCAACAATACATCG 973
Db 1079 ACAGGTGTAGCTGACTATATCTGGAGAAAACAGCGTTACATCTCTAGAAAACATTTGCC 1138
Qy 974 ACAACGCGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTTCGCGAGGACTTACC 1033
Db 1139 TCCGAAACAGGAGGAGCCCTCTATGGCAAAAAGATCTCTATAGATCTCTAATAATCTACA 1198
Qy 1034 CTATTCAGTAGAATAGTGTCAATGGAGGTACAGCTCCTTAAAGGTGAGGCAATGCTATC 1093
Db 1199 ATATTTCTTTGGAAA-----TACAGCTGGAAAAGGAGCGCTATTGCTATT 1243
Qy 1094 GAAGATAGTCGGGAATTTAGTTTATCCGCGATAGTGGTACACATTTGCTTTTATAGGGAAT 1153
Db 1244 CCGGAATCTGGGAGCTCTCTATCCGAAATCAAGGTGATATCTCTTTTAAACAAGAC 1303
Qy 1154 ACAGTCACTTCTACTACTCTCTGGGACGAATAGAGTAGTAGTACGATTTAGGAACGAGTGCA 1213
Db 1304 C---TCAGCATCACTAGTGGGACACCTACTCTCGCAATAGTATTCACTTCGAAAAGATGCC 1360
Qy 1214 AAGATGACAGCTTTGCGTTCTGCTGTGGTGGAGCCATCTACTTCTATGATGCCATAACT 1273
Db 1361 AAGTTTGCCACTCTAGGGAATAGCAAGGCTATACCCCTACTTCTTCTATGATCGGATTACA 1420
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Qy 1274 ACAGGATCATCCCAACAGTTACAGATGTCTTAAAGCTTAAAGACTCCGCGAGATTCT 1333
Db 1421 TCTGATGATTATCTGCTGCAATCCGACGCGCTACTGTGTGTCATTTCTTCCAAACCCAGT 1480
Qy 1334 GCA---CTACAATATACAGGGAACATCATCTTCAAGGAGAAAAGTTTATCAGACACAGAG 1390
Db 1481 GCAGATGGTGGTATTCAGGAGACTATTTGTTCTTTTTCAGGAGAAACCCCTCACTGCTACCGAA 1540
Qy 1391 GCGCGAGATTCTAAAATCTTACTTTCGAAGCTACTACAGCTGTGTAATCTTTTCAGGAGGT 1450
Db 1541 GCAGCAACCCCTGCAATGCTACATCTACATTTAAACCAAAAGCTTAGAACTTTGAAGCGGT 1600
Qy 1451 ACTCTATCTTTAAAACATGAGTGTCTCTCGAGCTCAGGACTCAGGCACTTCACTCAACAGGAGAT 1510
Db 1601 ACTCTGCTTTTAAAGAACGGTGTCTTAAATGTTTCATTAACCTTTCACGCAAGATGAAAG 1660
Qy 1511 TCTCGTCTCGAAATGGACGTAGGAATCTCTTAGAACCTCGTGATA----- 1556
Db 1661 TCGTCTCATCATGATGATGCGAGGACCACTTAGCACTACAAATGGAGCTAATAACT 1720
Qy 1557 -----CTAGACCATATAACAATTTGGTTCATTAAACATCAGTTCCTATAGACGGTGCAAG 1609
Db 1721 GACGGTCTATCACCTTAAACAAGCTTGTAAATCAATCTGGAATCTTTGGATGGCACTAAA 1780
Qy 1610 AAGGCAAAATAGAAACCAACCAAGCTACGTCAAAAATCTGACTTTTATCTGAAACCATCACT 1669
Db 1781 GCGGCTGTCTTAATGTGCAGATACCAATGGAGCTCTCACTATATCCGGAATTTAGGA 1840
Qy 1670 TTATTGGACCGGACGGGACGTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCCTAC 1729
Db 1841 CTGTGAAAACACTCTCAAGATTGCTGTGACAAACCAAGGATGTTTAAAGATTTCACG 1900
Qy 1730 GAC-----ATCTTAGAGCTCAAAGCTTCTGGA---ACTGTAAACAACACCGCAGTCACT 1780
Db 1901 CAAAGTTCCGATTTTAGAACTCAAAGCGACTTCAAATACTGTAACCTACCGACTTCACT 1960
Qy 1781 CCAGATCCTATATGGTGGAATTTCCATTAAGGCTATCAGGCTATCAGGGAATTTGGGCCCCAAT 1840
Db 1961 CTCGGCACAAACCGGCTATCAGCAATCTCCCTATGGGTATCAAGGAACTTCGGGAGTTTACC 2020
Qy 1841 GTTTGGGGAGACGGGCTTCTACGACTGCAACCTTCAAAGTGGACTAAACCTGGGTATATT 1900
Db 2021 ATAGACAGCAACCACTACGGTCAAGGA-----AATTGGAAAACCAACCGGTTATCTT 2074
Qy 1901 CTTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTATAGAT 1960
Db 2075 CCTCATCCGAGCGTCTTGTCCCTCATTTCTTAATAGCTATGGGCAACCGTCATAGAT 2134
Qy 1961 ATTAGCTCTCTCCATTTCTTATGGAGACTGCAACGAAAGGTTGAGGAGACCGTGTCT 2020
Db 2135 TTACGAGCTGTAAGTCAAGCTCAGCGCTGATGGCGAAGATGTCCCTGGGAGAAC-- 2192
Qy 2021 TTTTGTGTCTGGAATATCTTAACCTTCTTCCATAAGGATAGTACAAAAACACACGCGGG 2080
Db 2193 -TGAGCATCACAGGAATTAACAATTTCTCCATCGCAATCATACCGGTGATGACGCGC 2251
Qy 2081 TTTTGGCAATTTAGTGGCGGTTTATGTCATAGGAGGAAACCTACATCTTGTTCAGATAAG 2140
Db 2252 TACCGCATATGGTGGAGGCTACCTCATCAATACCTACACAGGCATCACTCCAGATGCT 2311
Qy 2141 ATTTCTTAGTGTGCAATTTGTGAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAG 2200
Db 2312 GCGTTAAGTCTAGTTTGGACAGCTGTTTACAAAATCTAAGGATTAACCTCGTAGGTAC 2371
Qy 2201 AATCAAGGTACAGCTTACGAGGAACTCTCTATTACAGCAACCAACCACTTATCTCT 2260
Db 2372 GGTCACTTAAAGTTTATTTTCGTACAGTACTCTAAATC----- 2413
Qy 2261 CTTCTTGGCAACTACGGCTTGTTCGTTGTCTTATGTTCTTACAGAGATTCTGTCTTC 2320
Db 2414 -----ACCAAGTCTCTGTTTGGATCATCGAGATTCCTTCTCAGGAGGACCTTCTC 2462
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QY 2321 TTTTCAGGAACCTTTAGCTACACCATGATACGATACGATCTGAAACCAAGTATACAA 2380
DB 2463 GAG-----TTACCTATAGCGGTAGCAATGAGAAAGTAAAGACTTCATATCAAAA 2512
QY 2381 TATCCTACTGTTAAAGGAGCTGGGGGATGATAGTCTTTCGCTTTAGAAATTCGGTGAAGA 2440
DB 2513 TTGCCCTAAAGGCGCTGCTCTTGGAGTAACTAATGCTGGTTAGGAGAACTCGAAGGGAAC 2572
QY 2441 GCTCCGATTTGCTTAGATGAAGTCTCTA---TTTGAGCAGTACATGCCCTTCATGAAA 2497
DB 2573 CTTCCATCACTCTCTCTCTCGCATCTTAACCTCAAGCAGATCATTCCTTTGTAAAA 2632
QY 2498 TTGCGATTGTCATGCAATCAGGAAGTTTAAAGAACAGGGAACAGAACTCGTGAA 2557
DB 2633 GCTGAAGTTGCTTACGCGACTCATGGGGGCATCCAGAAATAACCCCGAGGGGAGATT 2692
QY 2558 TTGGAAGTAGCCGCTTTGTGATCTTGCCTTACCTATCGGATCCGATTTGATAGGAA 2617
DB 2693 TTGGAACAGGTCATCTACTCAACGTTCAGTTCCCGTAGGGCGTCCGCTTTGGTAAAT 2752
QY 2618 TCAGACTGCCAGATGCCAAGTACAACTCTTCTTGGTTTACTGTGGATCTTGTCTGT 2677
DB 2753 TCTCATATCGACAGATTTTACACTATAATCGTAGCCTATGCTCTATCTGT 2812
QY 2678 AGTAACCCGACTGTAGCAACACATCGCAATAGCGGTGATCTTTGAAAAACCTTCGGT 2737
DB 2813 CACAATCCCTGATTGGGATACGACATTAACCTTAAATGGAGCTACGTGGACCTCTATAGG 2872
QY 2738 ACGAATTTGGCAGACAGCTTTAGTCCCTTCGTCGAGGGAACCATTTTGTCTTAACCTCA 2797
DB 2873 AATAATCTAACAGAAATGTTTGTGTAGTACAAAGCATCCAGCAATCCAGCAATGAT 2932
QY 2798 AATTTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTCACTCGCAATACAA 2857
DB 2933 GTTCTAGAGATCTTCGGGACCTGTGGATGTGATATTCGCAGAACCTCCCGTAAATATCT 2992
QY 2858 GTAGACTTAGGAGCAAAATACCAATTTCTAATCGGT 2892
DB 2993 CTAGATATAGGAAGCAAAATTAGCAATTTAAACCTT 3027

RESULT 4
US-09-612-402B-23
; Sequence 23, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 3354
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
US-09-612-402B-23
Query Match 4.7%; Score 140.6; DB 4; Length 3354;
Best Local Similarity 48.5%; Pred. No. 6.2e-32;
Matches 549; Conservative 0; Mismatches 534; Indels 48; Gaps 4;
QY 1776 TGACTCCAGATCCATAAATGGGTGAGAAATTCATTTACGCTATACGGCTATCAGGAACTTGGGGCC 1835
DB 1970 TGACTCTAGGAATGAGATCCCTAAGTATGGCTATCAAGGAAGCTGGAAGCTTGGCGTGG 2029

QY 1836 CAATGTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAACCTGGCT 1895
DB 2030 ATCTTAATACAGCAAAATATGCTCTTATATCTCTGAAAGCTACATGGAATCTGGGT 2089
QY 1896 ATATTCCTAAATCCGAGCGTATCGGCTCTTTAGTCCCTAAATAGCTTATGGAATGCAATTTA 1955
DB 2090 AATAATCTGGGGCTGAGCGAGTAGCTCTTTGGTTCCAAATAGTTTATGGGGATCCAATTT 2149
QY 1956 TAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAAACGAAGGTTGCAAGGAGACC 2015
DB 2150 TAGATATACGATCTCGCAATTCAGCAATTCAGCAAGTGTGATGGGGCTCTTTATGTC 2209
QY 2016 GTGCTTTTGGTGTGCTGATATCTAATCTTCTCCATTAAGATAGTACAAAAACAGCAC 2075
DB 2210 GAGGATATGGGTTTCTGGAGTTTCGAATTTCTCTATCATGACCGCATGCTTTAGGTC 2269
QY 2076 GGGGTTTCGCCATTTGAGTGGCGGTATGTATAGGAGGAAACCTACATATCTGTTTCAG 2135
DB 2270 AGGATATCGGTATATTAGTGGGGTTATCTCTTAGGAGCAAACTCTTCTTGGATCA- 2328
QY 2136 ATAAATTTCTTAGTGTCTGATTTTGTCTAGCTCTTTTGGAGAGATAGAGACTTCTTGATG 2195
DB 2329 --TCGATGTTTGGTCTAGCAATTTACTGAATATTGTTGGTAGATCTAAAGATTATGATGT 2386
QY 2196 CTAAGATCAAGGTACGTCTACGGAGGAACCTCTCTATTTACCAGCACACGAACCTATA 2255
DB 2387 GTCTTCCCAATCATCATGCTTGCTAGGATCGGTTTATCTATCTACCAA----- 2435
QY 2256 TCTCTCTTCTTGCAAACTACGGCCTTGTTCGTTCTTATCTTCTTCTTCTACAGAGATTCCTG 2315
DB 2436 -----ACAGGCTTTATGTGGATCTTATGTGTTGGAGATGCGTTTA 2476
QY 2316 TTCTCTTTTACGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAAACAAGTATA 2375
DB 2477 TTC-----GTGCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2524
QY 2376 CAACATATCCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGTTTGAATTCGGTG 2435
DB 2525 CATTTGCAGAGGAGAGCGATGTTTGTGGGATAAATACTGTCTGGTTGGAGAGATGGAG 2584
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QY 2493 TGAATTTGAGTTTGTCTATGACATCAGGAAGGTTTAAAGAAACGGAACAGAGCTC 2552
DB 2645 TGCAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGCGGATCAAGCTC 2704
QY 2553 GTGAATTTGGAAGTAGCCGCTCTTGTGAATCTTGCCTTACCTATCGGATCCGATTTGATA 2612
DB 2705 GGGCATTCAGGAGTGACATCTCATGAATCTATCAGTTCTGTGGAGTAAATTTGATC 2764
QY 2613 AGGAATCAGACTGCCAAGATGCAACGTAACAATCTAATCTTGTGTTTACTGTGATCTTG 2672
DB 2765 GATGTTCTAGTACACACCCCTAATAATATAGCTTTTATGGGGCTTATATCTGTGATGCTT 2824
QY 2673 TTGCTAGTAAACCCGACTGTACGAACAACTCGGAATTAGCGGTGATTTCTGGAAACCT 2732
DB 2825 ATCGCACCATCTCTGGGACTCAGAACCACTCTCTATCCATCAAGAGAGATGAGCAACAG 2884
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTTGTAGTCTTCGTCGAGGAACCAATTTTGTCTTA 2792
DB 2885 ATGCTCTTTCATTTGGCAAGACATGGAGTATAGAGGTTCTATGATGTTCTCTAA 2944
QY 2793 ACTCAAAATTTGAAGCTTTTAGCCAAATTTTCTTTGAATTTGGTGGGTCACTTCGCAAT 2852
DB 2945 CAAGCAATATAGAGTATATGCGCAATGGAAGATATGAGTATCGAGATCTTCTCGAGGT 3004
QY 2853 ACATGTAGACTTAGGCAAAATACCAATTTCTAATGCGGTAGCTTTGGTA 2903
DB 3005 ATGTTTGTAGTGCAGGAAGTAAAGTCCGGTCTTAAATAATATTTGTTAGATA 3055

RESULT 5
US-09-612-402B-24
; Sequence 24, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 3324
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant Expression Vector
US-09-612-402B-24

Query Match 4.5%; Score 133.8; DB 4; Length 3324;
Best Local Similarity 48.7%; Pred. No. 7.2e-30;
Matches 551; Conservative 0; Mismatches 532; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGAACTTCAGGGAACTTGGGGCC 1835
DB 1973 TGACTCTAGGAATGAGATGCCCTAGTATGGCTATCAAGGAAGCTGGAAGCTTGGCGGG 2032

QY 1836 CAATTGTTGGGGCAGAGGGCTTCTACGACTCAACCTTCACTGACTTAAACCTGGCT 1895
DB 2033 ATCTTAATACAGAAATATATGTCCTTACTCTGAAGCTACATGACTTAAACCTGGGT 2092

QY 1896 ATATCTCTAATCCGAGCGTATGGCTCTTTAGTCCCTAATAGCTTATGGAAATGCAATTTA 1955
DB 2093 ATAACTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTATGGGATCCATTT 2152

QY 1956 TAGATATTAGCTCTTCCATATATCTTATGGAGACTGCAACGAAGGTGGCGGGAGACC 2015
DB 2153 TAGATATAGCATCTGGCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATGTC 2212

QY 2016 GTGCTTTTGGTGTGCTGATATCTAACTTCTTCCATAGGATAGTACAAAACAGAC 2075
DB 2213 GAGGATATGGGTTCTGGAGTTTCGAATTTCCCTATCATGCCGAGTCTTTAGGTC 2272

QY 2076 GCGGGTTTCCCATTTGAGTGGCGGTATGTCTAGGAGGAAACCTACATACCTTGTTCAG 2135
DB 2273 AGGGATATCGGTATATTAGTGGGGTTATCTCTAGGAGCAAACTCTACTTTGGATCA- 2331

QY 2136 ATAAGATCTTAGTGTGATTTTGTGAGCTCTTTGGAGAGATAGAGACTACTTTGTAG 2195
DB 2332 --TCGATGTTTGGTCTAGCAATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTG 2389

QY 2196 CTAAGAATCAAGGTACAGTCTACGGGAACTCTCTATTACCAGCACACGAAACCTATA 2255
DB 2390 GTGTTTCCAAATCATGCTTGCATAGGATC-----CGTTA 2426

QY 2256 TCTCTCTCTTGCAAACTACGGCTTGTTCGTTGTCTTATGTTCTACAGAGATTCCTG 2315
DB 2427 TCTATCTACAAACAAGCT-----TTATGTGGATCCTATTGTTCCGGATCGGT 2477

QY 2316 TTCTCTTTTCAGAAACCTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATA 2375
DB 2478 TATCCGT-----GCTAGTACGGGTTTGGGAACCAAGCATATGAAACCTCATACA 2527

QY 2376 CAACATATCCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTTGAATTCGGTG 2435
DB 2528 CATTCGAGAGGAGCGGATGTTCTGTTGGGATATAAATCTGTCGTGTGGAGATGGAG 2587

QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTCTCTATTGAGCAGTACATG---CCCTTCA 2492

DB 2588 TGGGATTACCGATGTGACTACTCCATCTAAGCTCTATTGAATGAGTTGCGCTCTTCG 2647
QY 2493 TGAATTTGCAAGTTTGTCTATGCACATCAGGAAGGTTTTTAAAGAACAGGAACAGAGCTC 2552
DB 2648 TGAAGCTGAGTTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGGCGATCAAGCTC 2707
QY 2553 GTGAATTTGGAAGTAGCCGCTCTGTGAATCTTGGCCCTTACCTATCGGATCCGATTTGATA 2612
DB 2708 GGGCATTTCAAGAGTGTCTCATCAATCTATCAGTTCCTGTTGGAGTAAATTTGATC 2767
QY 2613 AGGAATCAGACTGCCAAGATCAACCGTACAATCTAATCTTGTGTTATCTGTGTAATCTTG 2672
DB 2768 GATGTTCTAGTACACACCCCTAATAATATAGCTTTTATGGGGCTTATATCTGTGATGCTT 2827
QY 2673 TTGCTAGTAACCCGACTGTACGAACTGGAATAGCGGTGATTTCTTGGAACCT 2732
DB 2828 ATGCAACCATCTCTGGGACTCAGAACACCTCTATCCCATCAAGAGACATGAGCAACAG 2887
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTAGTCTCTTCGTCAGGGAACCAATTTTGTCTTA 2792
DB 2888 ATGCTTCTTATTTGGCAAGACATGGATCATAGTTAGGGTCTATGTTGTTCTCTAA 2947
QY 2793 ACTCAAATTTGAAGCTTTTAGCCAAATTTCTTTTGAATTTGGTGGGTCTATCTCGCAAT 2852
DB 2948 CAAGCAATATAGAAGTATATGCCCATGGAAGATATGAGTATCGAGATCTTCTCGAGGT 3007
QY 2853 ACATGTAGACTTAGGAGCAAAATACCAATTTCTTAATGCGTTAGCTTTGGTA 2903
DB 3008 ATGGTTTGAAGTGCAGGAAGTAAAGTCCGGTCTCTAAATAATTTGGTTAGATA 3058

RESULT 6
US-09-556-877-182
; Sequence 182, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Filing, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.489C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-182

Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.1e-29;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACCTTGGGGCC 1835
DB 1952 TGACTCTAGGAATGAGATGCGCTAAGTATGGCTATCAAGGAAGCTTGGGTGGG 2011
QY 1836 CAATTTGTTGGGGCAGGGGCTTCTACGACTGGAACCTTCACTGGAATAAATCTGGCT 1895
DB 2012 ATCTTAATACAGCAAAATATATGTTCTTATCTTACTCTGAAAGCTACATGGAATAAATCTGGGT 2071
QY 1896 ATATCTCTAATCCGAGCGTATCGGCTCTTATGTCCTTAATAGCTTATGTAATGCAATTTA 1955
DB 2072 ATAACTCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2131
QY 1956 TAGATATTAGCTCTCTCCATTTATCTTATGAGACTGCAACGAAGGTTTGCAGGAGACC 2015

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Db 2132 TAGATATACGATCTGCGCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATTGTC 2191
QY 2016 GTGCTTTTGTGCTGATTAATCTAATCTCTCCATAAGGATAGTACAAAAACAGAC 2075
Db 2192 GAGGATTAAGGTTCTGGAGTTTGAATTTCTTATCATGACCGCATGCTTTAGTCT 2251
QY 2076 GCGGTTTTCGCAATTTGAGTGGCGGTTATGTATAGAGGAAACCTCATACTTTGTCAG 2135
Db 2252 AGGATATCGGTATATATAGTGGGGTATTCTTAGGAGCAACTCTTACTTTGGATCA- 2310
QY 2136 ATAGATTTCTTAGTGTGCTCAATTTGTGCTCTTTGGAAGAGATAGAGTACTTTGTAG 2195
Db 2311 --TCGATTTTGGTCTAGCATTTACCGAAGTATTGTGTAGATCTAAAGATTATGTAGTGT 2368
QY 2196 CTAAGATCAAGGTACAGTCTACGGAGAACTCTATTACCAGCACAAACCAACTATA 2255
Db 2369 GTGCTTCAATCATCATGCTTTCATAGATC-----CGTTTA 2405
QY 2256 TCTCTCTTCTTTCGAAACTACGGCTTGTCTGTTGTCTTATGTTCTTCTTACAGAGATTCCTG 2315
Db 2406 TCTATCTACCAACAAGCT-----TTATGTGATCTCTATTGTTTGGAGATGCGTT 2456
QY 2316 TCTCTTTTTCAGAAACCTTAGCTACACCCATACGATAACGATCTGAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2506
QY 2376 CAACATATCTTACTGTTTAAAGAACTCGGGGAATGATGTTTCGTTTAGAAATTCGGTG 2435
Db 2507 CATTTGAGAGAGAGCGATGTTCTGGGATATTAATCTGCTGCTGGAGAGATTGGAG 2566
QY 2436 GAAGAGCTCCGATTTGCTAGATGAAGTGTCTTATTTGAGCAGTACATG---CCTTTCA 2492
Db 2567 CGGATTAACCGATTGTGATTAATCTCAATCAAGCTCTATTGAATGAGTTGGTCTCTTCG 2626
QY 2493 TGAATTCAGTTTCTATGATGATCAATCAGGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
Db 2627 TGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGAAAGCGGATCAAGCTC 2686
QY 2553 GTGAATTTGGAAGTAGCGCTGTTGGAATCTTGGCTTACCTATCGGGATCCGATTGATA 2612
Db 2687 GGGCATTCAGAGCGGACATCTCTTAATCTATCAGTTCTCTTGGAGTGAAGTTGATC 2746
QY 2613 AGGAATCAGCTGCCAAGATGCAAGTCAATCTAATCTTGTGTTTATCTGTGATCTTG 2672
Db 2747 GATGTTCTAGTACACATCTTAATAAATATAGCTTTATGCGGCTTATATCTGTGATGCTT 2806
QY 2673 TCGTAGTAAACCCGACTGTAGCAACACCTCGGAATTAGCGGTGATCTTTGGAAACCT 2732
Db 2807 ATCGCACCATCTCTGTTACTGAGAACACGCTCTATCCCATCAAGAGACATGGAACAG 2866
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTTAGTCTTCTGTCGAGGAAACCACTTTTTCCTTTA 2792
Db 2867 ATGCTCTTCAATTTAGCAAGACATGAGTTGTGTTTAGAGGATCTATGATGCTTCTCTAA 2926
QY 2793 ACTCAATTTTGAACCTTTAGCCAAATTTCTTTTGAATGCGTGGTCACTCCCAATT 2852
Db 2927 CAAGTAATATAGAGTATATGCGCATGGAAGATATGAGTATCGAGATGCTTCTCGAGCT 2986
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2987 ATGTTTGAGTGCAGGAAGTAAAGTCCGGTTCTAA 3021
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RESULT 7

US-09-620-412C-182

; Sequence 182, Application US/09620412C

; Patent No. 6448234

; GENERAL INFORMATION:

; APPLICANT: Steven P. Fling

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469C7

; CURRENT APPLICATION NUMBER: US/09/620,412C

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; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-182
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Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.1e-29;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;
QY 1776 TGACTCCAGATCCCTATATATGGGTGAGAAATTCCTATTACGGCTATCAGGAACTTTGGGGCC 1835
Db 1952 TGACTCTAGGAAATGAGATGCTTAAGTATGCTATCAAGGAAGCTTGAAGCTTTGGCTGGG 2011
QY 1836 CAATGTTTGGGGACAGGGCTTCTACGACTGCAACCTTCACTGGACTAAACCTGCT 1895
Db 2012 ATCTAATACAGCAAAATTAATGCTCTTATATCTCTGAAGCTACATGGACTAAACCTGGT 2071
QY 1896 ATATTCTAATCCCGAGCTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTA 1955
Db 2072 ATATCTCGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCAATTT 2131
QY 1956 TAGATATTAGTCTCTCTCCATTTCTTATGAGACTCTGCAACGAAAGGTTTCAGGGAGACC 2015
Db 2132 TAGATATACGATCTGCGCAATTCAGCAATTCAGCAAGTGTGATGGCGGCTCTTATTGCTC 2191
QY 2016 GTGCTTTTGTGCTGATTAATCTAATCTCTCCATAAGGATAGTACAAAAACAGAC 2075
Db 2192 GAGGATTAAGGTTTCTGAGTTCGAATTTCTTCTATCATGACCGCATGCTTTAGGTC 2251
QY 2076 GCGGTTTTCGCAATTTGAGTGGCGGTTATGTCATAGAGAGAAACCTCATACTTCTTCTCAG 2135
Db 2252 AGGATATCGGTATATATGTTGGGTTTATCTCTTAGAGCAACTCTTACTTTGGATCA- 2310
QY 2136 ATAGATTTCTTAGTGTGCTCAATTTGTGCTCTTTGGAAGAGATAGAGTACTTTGTTAG 2195
Db 2311 --TCGATTTTGGTCTAGCATTTACCGAAGTATTGTGTAGATCTAAAGATTATGTAGTGT 2368
QY 2196 CTAAGATCAAGGTACAGTCTACGGAGAACTCTCTATTACCAGCACAAACCAACTATA 2255
Db 2369 GTGCTTCAATCATCATGCTTTCATAGATC-----CGTTTA 2405
QY 2256 TCTCTCTCTTTCGAAACTACGGCTTCTTGTGTTCTTATGTTCTTCTTACAGAGATTCCTG 2315
Db 2406 TCTATCTACCAACAAGCT-----TTATGTGATCTCTATTGTTTGGAGATGCGTT 2456
QY 2316 TCTCTTTTTCAGAAACCTTAGCTACACCCATACGGAATACGATCTGAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2506
QY 2376 CAACATATCTTACTGTTTAAAGAACTCGGGGAATGATGTTTTCGTTTAGAAATTCGGTG 2435
Db 2507 CATTTGAGAGAGAGCGATGTTCTGGGATATTAATCTGCTGCTGGAGAGATTGGAG 2566
QY 2436 GAAGAGCTCCGATTTGCTAGATGAAGTGTCTTATTTGAGCAGTACATG---CCTTTCA 2492
Db 2567 CGGATTAACCGATTGTGATTAATCTCAATCAAGCTCTATTGAATGAGTTGGTCTCTTCG 2626
QY 2493 TGAATTCAGTTTCTTATGATGATCAATCAGGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
Db 2627 TGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGAAAGCGGATCAAGCTC 2686
QY 2553 GTGAATTTGGAAGTAGCGCTGTTGGAATCTTGGCTTACCTATCGGGATCCGATTGATA 2612
Db 2687 GGGCATTCAGAGCGGACATCTCTTAATCTATCAGTTCTCTTGGAGTGAAGTTGATC 2746
QY 2613 AGGAATCAGCTGCCAAGATGCAAGTCAATCTAATCTTGTGTTTATCTGTGATCTTG 2672
Db 2747 GATGTTCTAGTACACATCTTAATAAATATAGCTTTATGCGGCTTATATCTGTGATGCTT 2806
QY 2673 TCGTAGTAAACCCGACTGTAGCAACACCTCGGAATTAGCGGTGATCTTTGGAAACCT 2732
Db 2807 ATCGCACCATCTCTGTTACTGAGAACACGCTCTATCCCATCAAGAGACATGGAACAG 2866
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTTAGTCTTCTGTCGAGGAAACCACTTTTTCCTTTA 2792
Db 2867 ATGCTCTTCAATTTAGCAAGACATGAGTTGTGTTTAGAGGATCTATGATGCTTCTCTAA 2926
QY 2793 ACTCAATTTTGAACCTTTAGCCAAATTTCTTTTGAATGCGTGGTCACTCCCAATT 2852
Db 2927 CAAGTAATATAGAGTATATGCGCATGGAAGATATGAGTATCGAGATGCTTCTCGAGCT 2986
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2987 ATGTTTGAGTGCAGGAAGTAAAGTCCGGTTCTAA 3021
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Query Match 4.4%; Score 132.2; DB 4; Length 4435;
Best Local Similarity 48.6%; Pred. No. 2.7e-29;
Matches 550; Conservative 0; Mismatches 533; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCCTATATAGTGGTGAAGAAATCCCAATACCGCTATCAGGCTATCAGGAACTTGGGGCC 1835
DB 2351 TGACTCTAGGGAATGAGATGCTAAGTATGCTATCAAGGAAGCTTGAAGCTTGGCTGGG 2410

QY 1836 CAATTTGTTGGGGACAGGGCTTCTACGCTGCAACCTTCAACTGGACTAAACCTGGCT 1895
DB 2411 ATCTTAATACAGCAATTAATGCTTCTATATCTGAAGCTACATGGAATTAACCTGGT 2470

QY 1896 ATATTCCTAAATCCGAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTA 1955
DB 2471 ATATTCCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2530

QY 1956 TAGATATTAGCTCTCTCAATATCTTATGGAGACTGCAACGAAGGTTGAGGGAGACC 2015
DB 2531 TAGATATACGATCTGCGCAATTCAGCAATTCAGCAAGTGTGGATGGGCGCTCTTATGTC 2590

QY 2016 GTGCTTTTGGTGTGCTGGATATCTAACTTCTTCCATAAGGATAGTACAAAAACAGCAC 2075
DB 2591 GAGGATATGGTTCTGAGGTTTCGAATTTCTTCTATCATGACCGCGATGCTTTAGTGC 2650

QY 2076 GCGGTTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTGTTTCAG 2135
DB 2651 AGGGATATCGGTATATAGTGGGGTTATCTCTAGGCAAACTCTACTTTGGATCA- 2709

QY 2136 ATAGATTTTAGTCTGCTCAATTTGTGAGCTTTTGGAGAGATAGAGACTACTTTGTAG 2195
DB 2710 --TCGATGTTGGTCTAGCAATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 2767

QY 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAACCTCTATTACCAGCACAAACCAACTATA 2255
DB 2768 GTCTGTCATCATCATCTGTCATAGATC-----CGTTA 2804

QY 2256 TCTCTCTTCCTTGGAAATACAGGCTTGTGCTGCTTCTATGTTCTTCTACAGATTCCTG 2315
DB 2805 TCTATCTACCAACAAAGCT-----TTATGTGGATCCTATTGTTGGAGATGCGTT 2855

QY 2316 TTCTCTTTTCAGGAACCTTAGCTACACCCATACGATACGATACGATGAAACCAAGTATA 2375
DB 2856 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2905

QY 2376 CAACATATCTACTCTTAAAGAACTGGGGGAATGATAGTTTTCGCTTTAGAAATTCGGTG 2435
DB 2906 CATTTGAGAGGAGAGCGATGTTCTGTTGGATAATACTGTCTGCTGGAGATTTGAG 2965

QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATG---CCCTTCA 2492
DB 2966 CGGGATTAACCGATTGTGATTAATCTCAATCTAAGCTCTATTGGAATGAGTTGGTCTCTTCG 3025

QY 2493 TGAATTCAGTTTCTCTATGCATACAGGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
DB 3026 TGCAGCTGAGTTTCTTATGCGGATCATGATCTTTTACAGAGGAGCGGATCAAGCTC 3085

QY 2553 GTGAATTTGGAAGTAGCGCTCTTGTGAATCTTGCCTTACCTATCCGGATCCGATTTGATA 2612
DB 3086 GGGCAATCAAGAGCGGACATCTCTTAATCTATCAGTTCCCTGTTGGAGTGAATTTGATC 3145

QY 2613 AGGAATCAGATGCCAAGATGCAACGTACATCTAACTCTTGGTTTATCTGTGGATCTTG 2672
DB 3146 GATGTTCTTAGTACATCATCTTAATAATATAGCTTTATGGCGGCTTATATCTGTGATGCTT 3205

QY 2673 TTCGTAGTAAACCCGACTGTACGACACACTGCGAATTAGCGGTGATTTCTTGGAAACCT 2732
DB 3206 ATCGACCATCTCTGCTACTGAGACAAAGCTCTTATCCATCAAGAGACATGGACACAG 3265

QY 2733 TCGGTACGAATTTGGCAAGACTTTAGTCTCTTCTGTCGAGGGAACCAATTTTGCCTTA 2792
DB 3266 ATGCTCTTCAATTTAGCAAGACATGAGTTGTGGTTAGAGGATCTATGTATGCTTCTTAA 3325

QY 2793 ACTCAAAATTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGTTGGTCACTTCGCAAT 2852

Db 3326 CAAGTAATAGAAGTATATGCGCATGGAGATATAGTATCGAGATCTTCTCGAGGCT 3385
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTTAATGCGTTAGCTTTGGTA 2903
Db 3386 ATGGTTTGTAGTGCAGGAAGTAGAGTCCGGTTCTTAAATAATTTGTTAGATA 3436

RESULT 10
US-09-556-877-170
; Sequence 170, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469CS
; CURRENT APPLICATION NUMBER: US/09/556.877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-170

Query Match 4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 3.6e-29;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCCTATATAGTGGTGAAGAAATTCCTATACGGCTATCAGGAACTTGGGGCC 1835
DB 1880 TGACTCTAGGGAATGAGATGCTTAAGTATGCTATCAAGGAAGCTTGGAGCTTGGCTGGG 1939

QY 1836 CAATTTGTTGGGGACAGGGCTTCTACGCTGCAACCTTCAACTGGACTAAACCTGGCT 1895
DB 1940 ATCTTAATACAGCAATTAATGCTTCTTATATCTCTGAAGCTACATGGAATTAACCTGGT 1999

QY 1896 ATATTCCTAAATCCGAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTA 1955
DB 2000 ATATTCCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2059

QY 1956 TAGATATTAGCTCTCTCAATATCTTATGGAGACTGCAACGAAGGTTGAGGGAGACC 2015
DB 2060 TAGATATACGATCTGCGCAATTCAGCAATTCAGCAAGTGTGGATGGGCGCTCTTATGTC 2119

QY 2016 GTGCTTTTGGTGTGCTGGATATCTAACTTCTTCCATAAGGATAGTACAAAAACAGCAC 2075
DB 2120 GAGGATATGGTTCTGAGGTTTCGAATTTCTTCTATCATGACCGCGATGCTTTAGTGC 2179

QY 2076 GCGGTTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTGTTTCAG 2135
DB 2180 AGGGATATCGGTATATAGTGGGGTTATCTCTTAGGAGCAAACTCTCTACTTTGGATCA- 2238

QY 2136 ATAGATTTTAGTCTGCTCAATTTGTGAGCTTTTGGAGAGATAGAGACTACTTTGTAG 2195
DB 2239 --TCGATGTTGGTCTAGCAATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 2296

QY 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAACCTCTATTACCAGCACAAACCAACTATA 2255
DB 2297 GTGCTTCCATCATCATCTGCTTGCATAGATC-----CGTTA 2333

QY 2256 TCTCTCTTCTTGGAACTACAGGCTTGTGCTGCTTCTATGTTCTTCTACAGATTCCTG 2315
DB 2334 TCTATCTACCAACAAAGCT-----TTATGTGGATCCTTATTTGTTGGAGATGCGGT 2384

QY 2316 TTCTCTTTTCAGGAACCTTAGCTACACCCATACGGAATACGATCTGAAACCAAGTATA 2375
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Db 2385 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCTACTGTGTTAAAGGAAGCTGGGGGATGATAGTCTTCGCTTTAGAAATTCGGTG 2435
Db 2435 CATTTGAGGAGAGAGGATGTCGTTGGGATATTAACCTCTCGGCTGGGAGATTTGGAG 2494
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTCTCTATTTGAGCAGTACATG---CCCTTCA 2492
Db 2495 CGGGATTACCGATTGTGATTAAGTCTTAATTTGAATGAGTTGCGTCCCTTCG 2554
QY 2493 TGAATTTGCAATTTGCTATGCAATCAGCAAGAGGTTTAAAGAACAGGAAACAGAGCTC 2552
Db 2555 TGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGGCGATCAAGCTC 2614
QY 2553 GTCAATTTGGAAGTAGCGCTTTGTGAATCTTGCCTTACCTATCGGATCCGATTTGATA 2612
Db 2615 GGGCAITCAAGACGGACATCTCTAAATCTATCAGTTCTCTGTGGAGTAAATTTGATC 2674
QY 2613 AGGAATCAGACTGCCAAGATGCAACGTACAAATCTAATCTTTGTTTATCTGTGATCTTG 2672
Db 2675 GATGTTCTAGTACACATCTTAATAATATAGCTTTATGGCGCTTATATCTGTGATGCTT 2734
QY 2673 TTCGTAAGTACCCGACTGTACGACAACTGGAATTTAGCGGTGATTTCTGGAACACCT 2732
Db 2735 ATCGCACCTCTCTGTACTGAGACAAACGCTCTATCCCATCAAGAGACATGGAACAACAG 2794
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Db 2795 ATGCTTTCAITTAGCAAGACATGGAGTTGTGTTAGAGATCTATGATGCTTCTCTAA 2854
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Db 2855 CAAGTAATATAGAATATATGSCCATGGAAGATATGATATCAGATGCTTCTCGAGGCT 2914
QY 2853 ACATGATGACTTAGAGCAAAATACCAATCTAA 2887
Db 2915 ATGGTTTGAATGAGGAGMAGTAAGTCYGGTTCTAA 2949

RESULT 11

US-09-620-412C-170
; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-170

Query Match 4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 3.6e-29;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;
QY 1776 TGAATCCAGATCTATAATGGGTGAGAAATTCATTACGCTATCAGGAACTTGGGGC 1835
Db 1880 TGAATCCAGATGAGATGCTTAAGTATGGCTATCAAGAACTGGAAGCTTGGCTGGG 1939
QY 1836 CAATTTGTTGGGAGCAGGGGCTTCTACGACTGCAACCTTCAACTGAGCTAAACCTGGCT 1895
Db 1940 ATCTTAATACAGCAATAATGGTCCCTTATCTCTGAAGCTACATGACTAAACCTGGCT 1999
QY 1896 ATATTCCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
Db 2000 ATAATCCTGGGCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2059

QY 1956 TAGATATTAGTCTCTCCATTAATCTTATGAGACTGCAACAGAGGGTTGCAGGGAGACC 2015
Db 2060 TAGATATACATCTGGCAITTCAGCAATTCAGCAAGATGTGGATGGCGCTCTTATTGTC 2119
QY 2016 GTCTTTTGGTGTCTGGATTAATCTAACTTCTTCATAGAGTAGTACAAAACACGAC 2075
Db 2120 GAGGATTATGGGTTCTGGAGTTTCGAATTTCTTCTATCATGACCGGATGCTTTAGTCT 2179
QY 2076 GCGGGTTTCGCCAATTTGAGTGGCGGTATGTCTATAGGAGAAACCTTACATCTTGTTCAG 2135
Db 2180 AGGGAATCCGGTATATTAGTGGGGTTTATCTCTTAGGAGCAAACTCTACTTTTGGATCA- 2238
QY 2136 ATAAAGATTTCTAGTGTCTGATTTTGTCTCAGTCTTTTGGAGAGATAGAGTACTTTGTAG 2195
Db 2239 --TCGATGTTGGTCTAGCAATTTACCGAAGTATTTGGTAGATCTAAAGATTTATGTAGTGT 2296
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Db 2297 GTCGTTCCAATCATCATGCTTGCATAGGATC-----CGTTTA 2333
QY 2256 TCTCTCTTCTTGCAGAACTACGGCCTTGTGTGTTGCTTATGTTCTTACAGAGATTTCTCTG 2315
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QY 2316 TTTCTCTTTTTCAGGAAACCTTAGCTACACCACATACGATACGATCTGAAACCAAGTATA 2375
Db 2385 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCTACTGTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTG 2435
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Db 2615 GGGCAITTCAGAGCGGACATCTCTAAATCTATCAGTCTCTGTTGAGTCAAGTCTTATGATC 2674
QY 2613 AGGAATCAGACTGCGCAAGATGCAACGTAACAATCTCTTGTGTTATATCTGTGATGCTTGTG 2672
Db 2675 GATGTTCTAGTACACATCTCTAATAATAATATAGCTTTATGGCGCTTATATCTGTGATGCTT 2734
QY 2673 TTCGTAAGTAAACCCGACTGTACGCAACACTCGAATTTAGCGGTGATTTCTGGAACCT 2732
Db 2735 ATCGCACATCTCTGTACTGAGACAAACGCTCTATCCCATCAAGAGACATGGAACAACAG 2794
QY 2733 TCGGTACGAATTTGGCAAGCAAGCTTTTAGTCTCTGTCAGGGAACCAATTTTGTCTTA 2792
Db 2795 ATGCTTTCAITTAGCAAGACATGGAGTTGTGTTAGAGATCTATGATGCTTCTCTAA 2854
QY 2793 ACTCAAAATTTGAAGCTTTTAGCCAAATTTCTTTTGAATTTGGGTGATCTCGCAAT 2852
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QY 2853 ACATGATGACTTAGAGCAAAATACCAATCTAA 2887
Db 2915 ATGGTTTGAATGAGGAGMAGTAAGTCYGGTTCTAA 2949

RESULT 12

US-09-598-419-170
; Sequence 170, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John

;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
;; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;; FILE REFERENCE: 210121.459C6
;; CURRENT APPLICATION NUMBER: US/09/598,419
;; CURRENT FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 357
;; SOFTWARE: FastSeq for Windows Version 3.0/4.0
;; SEQ ID NO 170
;; LENGTH: 2949
;; TYPE: DNA
;; ORGANISM: Chlamydia
US-09-598-419-170

Query Match 4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 3.6e-29;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;
QY 1776 TGACTCCAGATCCCTAATATGGGTGAGAAATCCATTACGGCTATCAGGAACTGGGGCC 1835
DB 1880 TGACTCTAGGGAATGAGATGCTTAGTATGCTATCAAGGAAGCTTGAAGCTTGGCGGG 1939
QY 1836 CAATGTTTGGGGACAGGGCTTCTACGACTGCAACCTTCAACTGGACTAAACTGGCT 1895
DB 1940 ATCTTAATACAGCAATTAATGCTCTTATACCTCTGAAAGCTTACATGGACTAAACTGGGT 1999
QY 1896 ATATTCCTAATCCCGAGGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
DB 2000 ATATCCTGGGCTGAGCGAGTAGCTCTTTGGTTCCAAATAGTTTATGGGGATCAATTT 2059
QY 1956 TAGATATTAGCTCTCTCCATATCTTATGAGACTGCAAAAGGAGGTTGCGGAGACC 2015
DB 2060 TAGATATACGATCTCGCATTCAGCAATTCAGCAAGTGTGATGGGGCTCTTATTGTC 2119
QY 2016 GTGCTTTTGGTGTCTGCTGATATCTAATCTTCCATAAGGATAGTACAAAACAGCAC 2075
DB 2120 GAGGATTATGGTTTCTGAGTTTCGAATTTCTTATCATACCGCGAGTCTTAGGTGTC 2179
QY 2076 GCGGGTTTCGCCATTTGAGTGGCGGTATGTCATAGAGGAAACCTCATACTTCTTCAG 2135
DB 2180 AGGATATCGGTATATTAGTGGGGTATTCTTAGGAGCAACTCTTCTTGGATCA- 2238
QY 2136 ATAGAATCTTAGTGTGCTGATTTGTGCTAGCTCTTTGGAAGATAGAGACTTTGTAG 2195
DB 2239 --TCGATGTTGGTCTAGCATTTACCGAAGTATTTTGGTAGATCTAAAGATTATAGTGT 2296
QY 2196 CTAAGAACTCAAGGTACAGTCTACGAGGAACTCTTATTACGAGCACACGAAACCTATA 2255
DB 2297 GTCGTTCCATCATCATGCTTGCATAGATC-----CGTTA 2333
QY 2256 TCTCTCTTCCTTTGCAAACTACGGCCCTTGTTCGTTCTTATGTTCTCTACAGAGATTCCTG 2315
DB 2334 TCTATCTACCAACAAGCT-----TTATGTGATCCTATTGTTTCGGAGATCGGTT 2384
QY 2316 TTCTCTTTTCAGAAACCTTAGCTACACCCATACGATTAACGATCTGAAACCAAGTATA 2375
DB 2385 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCCTACTGTTAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATCGGTG 2435
DB 2435 CATTTGCAGAGAGAGCGATGTTGTTGGGATTAATACCTGCTGCTGAGAGATGGAG 2494
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTCTCTATTGAGCAGTACATG---CCCTTCA 2492
DB 2495 CGGGATTACCGATTGGATTACTCCATCTAAGCTCTATTGGAATGAGTTGCGTCTCTTGG 2554
QY 2493 TGAATTTGAGTTTGTCTATGATCAGATCAGGAGGTTTAAAGAACAGGGAACAGAGCTC 2552
DB 2555 TCGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGCGGATCAAGCTC 2614
QY 2553 GTGAATTTGGAAGTACCGTCTGTGAATCTTGGCTTACCTATCGGAGTCCGATTTGATA 2612
DB 2615 GGGCATTCAGAGCGGACATCTCTTAATCTATCAGTTCTCTGTTGGAGTTGATC 2674

QY 2613 AGGAATCAGACTGCCAAGATGCAAGCTACAACTTAACCTTCTGTTTATTAATGATGTC 2672
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QY 2673 TTGCTAGTAAACCCGAGTGTACGACACACACATGCGAATTTAGCGGTGATTTCTTGGAAACCT 2732
DB 2735 ATCGACCATCTCTGGTACTGAGACACGCTCTTATCCATCAGAGACATGGACAACAG 2794
QY 2733 TCGGTAGCAATTTGGCAAGACAACTTTAGTCTCTTGTGAGGGAACCAATTTTTCCTTTA 2792
DB 2795 ATGCTTTTCAITTTAGCAAGACATGAGTTGTGTTAGAGGATCTATGTATGCTTCTCTAA 2854
QY 2793 ACTCAATTTTGAAGCCTTTAGCCAAATTTCTTTGAAATGCGTGGGTCTCATCCCAAT 2852
DB 2855 CAAGTAAATATAGAATATATGCGCATGGAAGATATAGTATCGAGATGCTTCTCGAGCT 2914
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
DB 2915 ATGTTTGAAGTGCAGGAGTAAAGTCYGGTTCTTAA 2949

RESULT 13
US-09-612-402B-11
; Sequence 11, Application US/09612402B
; Patent No. 6642023
; GENERAL INFORMATION:
; APPLICANT: Jackson, W. James
; APPLICANT: Pace, John
; TITLE OF INVENTION: Chlamydia Protein, Gene Sequence and Uses Thereof
; Patent No. 6642023
; FILE REFERENCE: 7969-086-999
; CURRENT APPLICATION NUMBER: US/09/612,402B
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/942,596
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Chlamydia sp.
US-09-612-402B-11

Query Match 4.4%; Score 130.6; DB 4; Length 1444;
Best Local Similarity 48.7%; Pred. No. 3.9e-29;
Matches 543; Conservative 0; Mismatches 524; Indels 48; Gaps 5;
QY 1776 TGACTCCAGATCCCTAATATGGGTGAGAAATCCATTACGGCTATCAGGAACTTGGGGCC 1835
DB 375 TGACTCTAGGGAATGAGATGCTTAAGTATGGCTATCAAGGAAGCTTGAAGCTTGGTGGG 434
QY 1836 CAATTTGTTTGGGGACAGGGCTTCTACGACTGCAACCTTCAACTGGACTAAACTGGCT 1895
DB 435 ATCTTAATACAGCAATTAATGCTCTTATCTCTGAAAGCTACATGGAATAAACTGGGT 494
QY 1896 ATATTCCTAATCCCGAGGATTCGGCTCTTTAGTCCCTAATAGCTTATGGAATGATTTA 1955
DB 495 ATATTCCTGGGCTGAGCGAGTAGCTTCTTTGGTTTCCAAATAGTTTATGGGATCCATTT 554
QY 1956 TAGATATTAGCTCTCTCCATTTCTTATGAGACTGCAAAAGGTTTGCAGGGAGACC 2015
DB 555 TAGATATACGATCTCGCATTCAGCAATTCAGGAAGTGTGATGGCGCTCTTATTGTC 614
QY 2016 GTGCTTTTGGTGTGCTGATTAATCTAATCTTCCATAAGGATAGTACAAAACAGCAC 2075
DB 615 GAGGATTATGGTTTCTGGAGTTTCGAATTTCTTCTATCATGACCGGATGCTTTAGGTC 674
QY 2076 GCGGGTTTCGCCATTTGAGTGGCGGTATGTCATAGGAGGAACCTACATCTTGTTCAG 2135
DB 675 AGGGATATCGGTATATTTAGTGGGGTATTTCTTAGGAGCAAACTCTCTATTGGATCA- 733
QY 2136 ATAGAATCTTAGTGTGCTGATTTGTGCTCTTTGGAAGAGATAGAGACTACTTTGTAG 2195

Db 734 --TCGATGTTTGGTCTAGCATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 791
QY 2196 CTAAGAATCAAGGTACAGTCTACGAGGAACTCTCTATTACCAGCACAAACCACTATA 2255
Db 792 GTCGTTCCATCATCATGCTTGCATAGATC-----CGTTTA 828
QY 2256 TCTCTCTTCTTGGAACTACGGCTTGTTCGTTGTCTTATGTTCTTACAGAGATTTCCTG 2315
Db 829 TCTATCTACCCACAAGCT-----TTATGTGGATCCTATTGTTGGAGATGCGTT 879
QY 2316 TTCTCTTTTCCAGGAACCTTAGCTACACCCATACGATTAACGATTAACGATCTGAAACCAAGTATA 2375
Db 880 TATCCGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 929
QY 2376 CAACATATCCTACTGTTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTG 2435
Db 930 CATTTGCAGAGAGAGCGAUGTTCTGTGGGATTAATACGTCTCGCTGGAGAGATGGAG 989
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATG---CCCTTCA 2492
Db 990 CGGATTAACGATTTGATTACTCCATCTAAGCTCTATTTGAATGAGTTGGTCTCTTCG 1049
QY 2493 TGAATTTGCAGTTTGTCTATGCACATCAGGAGGTTTAAAGAACAGGGAACAGAGCTC 2552
Db 1050 TGCAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAAGCGATCAAGCTC 1109
QY 2553 GTGAATTTGGAAGTAGCGCTTCTGTAATCTTGTGCTTACCTATCGGGATCCGATTTGATA 2612
Db 1110 GGGCAITTCAGAGCGGACATCTCTAATCTATCAGTCTCTGTTGGAGTGAAGTTGATC 1169
QY 2613 AGGAATCAGACTGCGAAGATGCAACGTACAACTCTTGTGTTATCTGTTAGTGTGATCTTG 2672
Db 1170 GATGTTCTAGTACACATCTTAATAATATAGCTTTATGGCGCTTATATCTGTGATGCT 1229
QY 2673 TTGCTAGTAAACCCAGCTGTACGACACACCTGCGAAATAGCGGTGATCTTTGGAAACCT 2732
Db 1230 ATGCAACCATCTCTGTTACTGAGACAAACGCTCTATCCATCAAGAGACATGGACAACAG 1289
QY 2733 TCGGTACGAAATTTGGCAAGCAAGCTTTAGTCCCTTGTGAGGAGCAACATTTTGTCTTA 2792
Db 1290 ATGCTTTCAITTAGCAAGACATGGAGTTGGTTAGAGATCTATGTATGCTTCTCTAA 1349
QY 2793 ACTCAAAATTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTGATCTCGCAAT 2852
Db 1350 CAAGTAATATAGAAGTATATGGCCATGGAAGATATGATGAGATGCTCTCGAGGCT 1409
QY 2853 ACATGTAGACTTAGGAGCAAAATACCAATCTTAA 2887
Db 1410 ATGCTTTGAGTGCAGGAAGTAGATCGCGTTCTTAA 1444

RESULT 14

US-09-427-533B-1

; Sequence 1, Application US/09427533B

; Patent No. 6649370

; GENERAL INFORMATION:

; APPLICANT: Mordin, Andrew D.

; APPLICANT: Comen, Raymond P.

; APPLICANT: Dunn, Pamela L.

; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND

; FILE REFERENCE: 19721-009

; CURRENT APPLICATION NUMBER: US/09/427,533B

; PRIOR FILING DATE: 1999-10-26

; PRIOR APPLICATION NUMBER: 60/106,046

; PRIOR FILING DATE: 1998-10-28

; PRIOR APPLICATION NUMBER: 60/132,271

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 3050

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (101)..(2893)

US-09-427-533B-1

Query Match

Best Local Similarity 2.0%; Score 61.2; DB 4; Length 3050;

Matches 181; Conservative 0; Mismatches 173; Indels 6; Gaps 1;

QY 2484 TGCCCTTCATGAATTCAGTTTGTCTATGACATCAGGAGGTTTAAAGAACAGGGA 2543

Db 2487 TTCCTTTGTAGAACCGGATGATGTCGTATAGATCTTCCAGAAATTAGCGAACAGGGA 2546

QY 2544 CAGAGCTCGTGAATTTGGAAGTAGCGCTTGTGTAATCTTGCCTTACCTATCGGATCC 2603

Db 2547 AAGAGGTTAGAACGTTCCAAAAAATCTGTTTGAAGATGTGCCAATCTCTTTTGGATTG 2606

QY 2604 GATTGTATAAGGAATCA-----CACTGCCAAGATGCAACGTACAACTCTAACTCTTGTT 2657

Db 2607 CTTTAGACATGCTTATTCGGTGGCTCACGTGCTGAAGTGAACAGTGTACAGTTGCTT 2666

QY 2658 ATACTGTGGATCTTGTGTTAGTAAACCCGACTGTACGACAACTCGGAATTAGCGGTG 2717

Db 2667 ACGTCTTTGATATATCGTAAAGGACCTGTCTCTTTGATTACACTCAAGGATGCTGCTT 2726

QY 2718 ATCTTGGAAACCTTCGGTACGAAATTTGGCAAGACAGCTTTAGTCTCTTCTCGCAGGA 2777

Db 2727 ATTCTTGGAAAGATTATGGGGTAGATATCTTGTAAAGCTTGGAAAGCTCGCTTTGAGCA 2786

QY 2778 ACCATTTTGTCTTAATCAAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTTGGTG 2837

Db 2787 ATAATACGGAATGGAATTCATATTAAGTAGCTATTTAGCGTTTAATATGATGGAGAG 2846

RESULT 15

US-09-556-877-169

; Sequence 169, Application US/09556877

; Patent No. 6432916

; GENERAL INFORMATION:

; APPLICANT: Probst, Peter

; APPLICANT: Bhatia, Ajay

; APPLICANT: Skeiky, Yasir

; APPLICANT: Fling, Steve

; APPLICANT: Maisonneuve, Jeff

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; FILE REFERENCE: 210121.469C5

; CURRENT APPLICATION NUMBER: US/09/556,877

; NUMBER OF SEQ ID NOS: 305

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 169

; LENGTH: 2643

; TYPE: DNA

; ORGANISM: Chlamydia

US-09-556-877-169

Query Match

Best Local Similarity 1.7%; Score 50.6; DB 4; Length 2643;

Matches 122; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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Db 1218 AGAAGAAAAAATCTCTGATAAATCTTCCCACTACAGCAGCCTATCGAACTGAAATC 1277

QY 1447 AGGTACTCTATCTTTAAACATCGAGTACTGCGAGACTCAGGCATTCACCTCAACAGGC 1506

Db 1278 CGGACGCTAGTTTAAAGATCGCGTGTCTTTCCGCCCTTCTCTCTCTCAGGATCC 1337

QY 1507 AGATTCCTGCTCGAAATGGACGTAGGAATCTACTAGAACCTGCTGATAGTACCAT 1566

Db 1338 TCAAGCTCTCTCATTTATGGAAGCGGAACTTCTTTAAAAAATCTCTCTCTGATTTGAGTT 1397

Tue Aug 17 09:45:48 2004

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Qy	1627	C	1627	
Db	1458	C	1458	

Search completed: August 16, 2004, 18:46:29
Job time : 171 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 18:43:38 ; Search time 906 Seconds
(without alignments)
16247.045 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

Sequence: 1 cgcctctacctagtagaggt.....tggttgctaaacacttcc 3000

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303934 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3000	100.0	3000	10	US-09-428-122-1
2	2975.4	99.2	1230025	16	US-10-289-762-1
3	2241	74.7	2241	16	US-10-312-273-20
4	546.6	18.2	2781	10	US-09-738-269-56
5	546.6	18.2	2781	14	US-10-023-437-56
6	527	17.6	2787	16	US-10-312-273-96
7	523	17.4	534	16	US-10-312-273-18
8	516.6	17.2	2787	16	US-10-312-273-34
9	514	17.1	2793	13	US-10-282-122A-18496
10	514	17.1	2793	16	US-10-312-273-46
11	509.8	17.0	1230025	16	US-10-289-762-1
12	506.6	16.9	3050	9	US-09-452-380-1
13	506.6	16.9	3050	15	US-10-324-129-1
14	503.6	16.8	2811	13	US-10-282-122A-18495

15	503.6	16.8	2811	16	US-10-312-273-154	Sequence 154, Appl
16	477	15.9	2808	9	US-09-452-380-2	Sequence 2, Appli
17	477	15.9	2808	15	US-10-324-129-2	Sequence 2, Appli
18	465.8	15.5	2787	13	US-10-282-122A-18497	Sequence 18497, A
19	465.8	15.5	2787	16	US-10-312-273-116	Sequence 116, Appl
20	348.4	11.6	2520	10	US-09-738-269-22	Sequence 22, Appl
21	348.4	11.6	2520	14	US-10-023-437-22	Sequence 22, Appl
22	345	11.5	2526	13	US-10-282-122A-18493	Sequence 18493, A
23	345	11.5	2526	16	US-10-312-273-140	Sequence 140, Appl
24	289	9.6	1085	16	US-10-312-273-16	Sequence 16, Appl
25	284	9.5	1188	16	US-10-312-273-22	Sequence 22, Appl
26	271.8	9.1	2950	9	US-09-886-468-6	Sequence 6, Appli
27	271.8	9.1	2950	13	US-09-889-468-6	Sequence 6, Appli
28	270.6	9.0	2769	16	US-10-312-273-42	Sequence 42, Appl
29	243.4	8.1	3150	17	US-10-352-618-1	Sequence 1, Appli
30	243.2	8.1	2922	16	US-10-312-273-4	Sequence 4, Appli
31	218	7.3	4224	9	US-09-841-132-486	Sequence 486, App
32	218	7.3	4224	13	US-10-282-122A-18494	Sequence 18494, A
33	218	7.3	4224	16	US-10-312-273-32	Sequence 32, Appl
34	148.2	4.9	487	10	US-09-738-269-54	Sequence 54, Appl
35	148.2	4.9	487	14	US-10-023-437-54	Sequence 54, Appl
36	140.6	4.7	3354	13	US-10-701-844-23	Sequence 23, Appl
37	140.6	4.7	3354	17	US-10-766-711-23	Sequence 23, Appl
38	135.4	4.5	3042	17	US-10-467-534-10	Sequence 10, Appl
39	133.8	4.5	3324	13	US-10-701-844-24	Sequence 24, Appl
40	133.8	4.5	3324	17	US-10-766-711-24	Sequence 24, Appl
41	132.2	4.4	3021	9	US-09-841-132-182	Sequence 182, App
42	132.2	4.4	4435	13	US-10-701-844-1	Sequence 1, Appli
43	132.2	4.4	4435	17	US-10-766-711-1	Sequence 1, Appli
44	131.4	4.4	2949	9	US-09-841-132-170	Sequence 170, App
45	130.6	4.4	1444	13	US-10-701-844-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

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US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPED: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)...(2884)
US-09-428-122-1

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Query Match 100.0%; Score 3000; DB 10; Length 3000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db ||||| 180
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Db 361 AGGTAACGGGAACCTCTTATTTGTTCCAAACGGTGGATGAGGGAATGAGAGGGGCTGC 420
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RESULT 2
US-10-289-762-1
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
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; ORGANISM: Chlamydia pneumoniae
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RESULT 4

US-09-738-269-56

; Sequence 56, Application US/09738269

; Publication No. US20030185848A1

; GENERAL INFORMATION:

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; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
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; TYPE: DNA
; ORGANISM: Chlamydia psittaci
; US-09-738-269-56
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Query Match 18.2%; Score 546.6; DB 10; Length 2781;
Best Local Similarity 53.7%; Pred. No. 6.2e-144;
Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

QY 328 TTTTAAACACACTAAGGCGAATTTGACTTTTACAGGTAAACGGAACCTCTATTGTTTCCA 387
Db 231 TTTTGTTCAGACTGCAGACAACTAACTTTCAAAGGGAACAACCATAGCTTATCCATAAC 290
QY 388 AACGTTGGATGCGAGGACTGTAGCAGGGGCTGCTGTTTAAACAGCAGCGTGTAGATAATC 447
Db 291 GAACGCGGAATGCGGAGCTAATCC---TGCGGGAATTAACGTTAAACACTCCGATAAGAT 347
QY 448 TACCACCTTTATAGGGTTTCTTCGCTATCTTTTATTCGCTCTCTCGGAAGTTTCGATAAC 507
Db 348 TCTTACGCTCAGAGATTTTCTTAAGTTGAGCTTTAAGAAATGCCATCTCTCTTAGTGAA 407
QY 508 TACCGGCAAAAGGACCGTTAGCTGCTCTACGGTAGCTTGAGTTTGACAAAAAATGTCAG 567
Db 408 TACTGAAAAAGGGC---TATGAAATCCGGAGGAGCATTAACCTTAGCGAATAATGCCAG 464
QY 568 TTTGCTCTTCAGCAAAACHTTTTCAACGGATATGCGGTGCTATCACCGCAAAAACCTCT 627
Db 465 TATTCTGTTTGAATCAGAACTATTCCGCTGAGAAATGTTGGAGCCATCTCTTTCGAAAGCTTT 524
QY 628 TTCATTAAACAGGACTACAAATGTCAGCTCTGTTTCTGAAAAATACCTCTCAAAGAAAG 687
Db 525 TTCTCTAACCGGCTCGAGCAAAAGAAATCAGCTTCAACACTACTCTACTCGGAAAAAAGG 584
QY 688 CGAGCGCAATTCAGACTTCGATGCCCTTACCATTTACTTGGAAACCAAGGGGAAGTCTCTT 747
Db 585 TGGAGCGATTGCTGCTACGGGAATAGCTCATCTTCGACAAACCAAGGCACAAATCAGATT 644
QY 748 TTCTGACAACTACTCTTCGGAATTCGAGCTGCAATTTTACAGAACCTTCGGTGACTAT 807
Db 645 TTCTGGGAAACACTGCTGTGAAATTCGCGGAGCAGTATATTTCAGAAAGCTTCTATGACAT 704
QY 808 TTCTAATAATGCTAAAGTTTCTTATTTGACATAAAGTCAAGGTCAAGGACGAGCTCCTCAAC 867
Db 705 TGCAAGTAACAACAGTGTGCTTTTACCAACAATGCTGTTTCCGGTTCATCT----- 756
QY 868 AACGGGGATATGCTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAGGT 927
Db 757 -----GATGGTTGCGGTGGAGCTATCCATTTAGCAAAAACAGGTTTCAGCACCGACCT 809
QY 928 CACCCTCCTCGGAAATCAGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGAGG 987
Db 810 TACTATAAGAGATAACAAGTCTTGAATTTTGGAGAAAAATACTTCTTCAGCAAAAAGGTG 869
QY 988 AGCTATCTATGTGAAAAAGCTCGAACTGCTCCCGAGGACTTTACCTTATTCAGTAGAAA 1047
Db 870 AGCGATTACCGGATAAATCTCATATTGACTTCTGGTGGGCTTACGGCATTTTATCAATAA 929
QY 1048 TAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATATCGAAGATAGTGGGA 1107
Db 930 CAAAGTTACCCATGCTACA---CCTAAGGTGGAGCTATTGGTATTGCTGCCAATGAGA 986
```


TYPE: DNA
ORGANISM: Chlamydia psittaci
US-10-023-437-56

Query Match 18.2%; Score 546.6; DB 14; Length 2781;
Best Local Similarity 53.7%; Pred. No. 6.2e-144;
Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

QY 328 TTTTAAACACACTAAGGGCGATTGACTTTCACAGGTAAACGGGAACCTCTATTGTTCCA 387
DB 231 TTTTGTTCAGACTCAGACAACTTAACCTTTTCAAGAGGAACAAACATAGCTTATCCATAAC 290
QY 388 AACGGTGGATGACAGGAGCTGTAGCAGGGGCTGTGTTAAACAGCAGCGTGGTAGATAAATC 447
DB 291 GAACGGGAATGCGGAGCTAATCC--TGGCGGAATTAACGTTAACTGCCGATAGAT 347
QY 448 TACACGTTATAGGGTTTCTTCGCTATCTTTTATTTGCGTCTCCTGGAAGTTGATAAC 507
DB 348 TCTTACGCTGACAGATTTTCTAAGTTGAGCTTTAAGGAATGCCCATCTTCTCTAGTGA 407
QY 508 TACGGCAAAAGGAGCCGTAGCTCTACGGGTAGCTTGAGTTTGACAAAAATGTCAG 567
DB 408 TACTGGAAGAGGGC---TAGAAATCCGAGGAGCAATTAACCTTAGCGAATATATGCCAG 464
QY 568 TTGTGCTCTTCAGCAAAAACCTTTTCAACGGGATATGGCGGTGCTATCACCGCAAAAACCTCT 627
DB 465 TATTCTGTTGATCAGAACTATTCGCTGAGATGGTGGAGCCATCTCTTGCAGAGCTTT 524
QY 628 TTCAATTAACAGGACTCAATATGTCAGCTGTGTTTTCTGAAATACTCTCTCAAGAAAGG 687
DB 525 TTCTCTAACCGGCTCGAGCAAGAAATCAGCTTCACCACTAACTCTACTGCGAAAAAGG 584
QY 688 CGGAGCCATTACAGACTTCGATGCCCTTACCTACTGGAACCAAGGGGAGTCTCTTT 747
DB 585 TGAGCGCATGCTGCTACCGGAATPAGCTCACTTTTCGGAACCAAGGCAATCAGATT 644
QY 748 TTCTGCAATPACTTCTTCGGAATCTGAGGCTGCAATTTTACAGAACCTCGGTGACTAT 807
DB 645 TTCTGGGAACACTGCTGTGAATTCGGGGAGCAGTATATTTCAGAACTTCTATGACGAT 704
QY 808 TTCTAATAATGCTTAAGTTTCTTTATGCAATPAGGTCAAGGACGAGCTCTCAAC 867
DB 705 TGCAGGTAAACCAACCCGCTTCTTTAGCAACAATGCTGTTTCCGGTTCACTCT----- 756
QY 868 AACGGGGATATGTCAGAGGTGCTATCTGCTTATAAAGTACTAGTACAGATAAGT 927
DB 757 -----GATGGTTGCGGTGAGCTATCCATGTGACAAACAGGTTTCAGCCGACCC 809
QY 928 CACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCGCAACACAGCGGAGG 987
DB 810 TACTATAAGAGATAACAAAGTCTTGATTTTGGAGAAATACTTCTTCAGCAAAAGGTGG 869
QY 988 AGCTATCTATGTGAAGTCTGAACTGGCTTCGGAGGCTTACCCTATTCAGTAGAAA 1047
DB 870 AGCGAATTAACCGATAAATCATATTGACTTCTGTGGGCTCAGCGCAATTTATCAATA 929
QY 1048 TAGTGTCAATGGAGGTACAGCTCTCTAAAGTGGAGCCATAGCTATCGAAGATGCGGA 1107
DB 930 CAAGTTACCAATGCTTACA---CTAAGGTGGAGCTATTGGTATTGCTGCCAATGGAGA 986
QY 1108 ATTGAGTTTATCCCGGATAGTGTGATGCTTTTATAGGAA---TACAGTCACTTC 1164
DB 987 ATGTAGCTTAACCGCTGAACATGGGATATTACTTTTGATAATAACCTGATGCCACACA 1046
QY 1165 TACTACTCTGGGAGCAATAGAGTAGTATCGACTTAGGAAACGAGTCCAAAGATGACAGC 1224
DB 1047 AGCAATATGCTACATAAAAAAGAAATGCCATTAACATTTGAAGGCAATGGTAAATTCGTC 1106
QY 1225 TTTCGCTGCTGCTGGTAGCCATCTACTTCTATGATGCCATACACTACAGATCATC 1284
DB 1107 CTTACGTGGAGCGTCTGGAAGACGATTTCTTCTATGATCCCTATCACAGTTG----- 1159
QY 1285 CACAACAGTTTACAGATGCTCTTAAAGTTAATGAGACTCCGGCAGATTTCTGCACATAA 1344

DB 1160 -----AAGTAATGCTGCTGATCTTCTCACTTTGAAATAAAGCTGAGGGTGAATAACGTA 1214
QY 1345 TACAGGAAACATCATCTTTCACAGGAGAAAAAGTTATACAGAGACAGAGCCGAGATTCTAA 1404
DB 1215 TAATGGAAAGTAATTTTTCAGGAGAAAAGCTCACTGAAGAACAAAGCTGCTGTGTGGGA 1274
QY 1405 AATCTTACTTTCGAAAGTACTACAGCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAA 1464
DB 1275 TAACCTTAAGACAACTTTACACAGCCTATCACTTTAGCTGCTGGTGAACCTTGTGTACG 1334
QY 1465 ACATGAGTGACTCTGCAGACTCAGGCAATTCACCTCAACAGCAGCATTTCTGCTCGAAAT 1524
DB 1335 CAGGGTGTGGAAGTAGAAGCAAAACAGTGTGCAACAGCAGGATCTTTTGATCTGAT 1394
QY 1525 GGAGTAGGAACCTACTCTA---GAACCTGCTGATCTAGCACCATAAACAAATTTGGTCA 1581
DB 1395 GGATGCAAGGCACAAAGTTATCCGCAAAAACAGAAAGATGCTACACTGACGAATCTGGCTAT 1454
QY 1582 TAACATCAGTTCTATAGACGGTGCAGAAAGGCAAAATAGAAACCAACAAAGCTAGCTCAA 1641
DB 1455 TAATCCGAATACCTTAGATGGGAAAAAATTCGCCGTAGTGCATGCCGTTCTGCTGGGA 1514
QY 1642 AATCTGACTTTTATCTGGAACCATCACTTTTATTGGACCCGACGGGCACGTTTATGAAA 1701
DB 1515 GAATGTGACTTTATCAGTGTCTATTGGCGTTATTGATCTTACAGGGAAGTTTATGAAA 1574
QY 1702 TCATAGTTTAAAGAAATCTCAGTCTCAGACATCTTTAGAGCTCAAAAGCTTCTGGAAC 1761
DB 1575 CCATAGCTTAATGATACGTTAGCTTTAGGAGGAATTCAACTTTCTGGGAAAGGTTCCGT 1634
QY 1762 AACAGCACCGCAGTGCATCCAGATCCTATAATGCGGTGAGAAATTCATTTACGGCTATCA 1821
DB 1635 GACAACAAACCAACGTCCTAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1694
QY 1822 GGGAAAC-----TTGGGGCCCAATGTTTGGGGGACAGGGGCTTCTACAGCTGC 1869
DB 1695 AGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1754
QY 1870 AACCTTCAACTGACTGAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1929
DB 1755 AATCTTTACCTGGAATAAAGACAGATATGTTCCAAATTCCTGAACTGCTGCTGCTGCTGCTGCT 1814
QY 1930 CCCTAATAGCTTATGNAATGATATAGATATAGCTCTCTCCATTTATCTTATGAGAC 1989
DB 1815 ACTCAATAGCTTTGGGATCTTTATAGATTTACGTTCTTATCAAGATGCTTTGGAACG 1874
QY 1990 TGCAAAACGAAGGTTGCTG---AGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2046
DB 1875 TAGTGTGATAGTATTTCTGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1934
QY 2047 CTTCCATAAGGATAGTACAAAAACAGACGCGGGTTTGGCCATTTGAGTGGCGGTTAAGT 2106
DB 1935 CTTCCATAAAGATCGGAATGCTGAAATTCGAAATTCGATCATATCAGTTCCGGATATGT 1994
QY 2107 CATAGGAGAACTACATATTTGTCAGATAGATTTCTTAGTGTGCTGCTGCTGCTGCTGCTGCT 2166
DB 1995 GTTAGGAGCCCAACAAATACCTCGAGAGAGGATTTCTTTAGTGTGGCTTTCTGTCTAGTT 2054
QY 2167 CTTTGGAGAGATAGAGACTTCTTGTAGTAAAGATCAAGGTACAGTCTTACCGAGGAAC 2226
DB 2055 ATTTGCAAAAGATAAGACTACCTTGTAGCAAGAGACGCGCAACAGCTCTATCGGGTTTC 2114
QY 2227 TCTCTATTAACAGCA-----CAACGAAACCTTATATCTCTTTCTTTGCAAACTACGGCC 2280
DB 2115 TGTATATTATCAGCATGTGAGCAAGTTTGTATGATCTCAGCGGTTATTTAATGGGCTAA 2174
QY 2281 TTGTT 2340
DB 2175 CAGCTGTT 2234
QY 2341 CACCCATAGCGATAACGATCTGAAAAACCAAGTATACAAATATCTTACTTGTTTAAAGGAAG 2400

Db 2235 TTGCGACACGGCCCAACATGACAACTGCTATATACAGACTATCTGAGTGAAAGGTTTC 2294
Qy 2401 CTGGGGGATGATAGTTTCGCTTTAGAAATCGGTGGAAGAGCTCCGATTTGCTTAGATGA 2460
Db 2295 TTGGGGATGATGATACCTGGGCTTAACCTTTGCTACTAGCGTACCTATCCCGGTATTTAG 2354
Qy 2461 AAGTCTCTATTGTAGCAGTACATGCCCTTCATGAAATTTGCAATTTGCTATGCAATCA 2520
Db 2355 TTCCTCTATCTTTGATGATGACCGCTTTGCAAAATTTACAAGTTGCTATGCGCACCA 2414
Qy 2521 GGAAGGTTTAAAGAACAGGGAAACAGAGCTCGTGAATTTGGAAGTAGCCGCTTTGTGAA 2580
Db 2415 AGATGACTTTAAAGAACCAACACAGAGCGCGGTCTTTGAAAGCAGCGATCTTCTCAA 2474
Qy 2581 TCTTCGCTTACCTATCGGATCCGATTTGATAAGGAATCAGACTGCAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACCTATAGGTATTAATAATTTGAGAAATCTCTCTATGAGAGAGAAGTCTTA 2534
Qy 2641 CAATCTAACTCTGTGTTTACTGTGTGATCTGTTTCTGTAGTAACCCGACTGTACGACAA 2700
Db 2535 TGATCTTACACTGATGATATACCTGATGTGACCGTCAATCCAAAGCTGTATGACAGG 2594
Qy 2701 ACTGGAATACCGGTGATCTTGTGAACCTTCGCTAGCAATTTGGCAAGCAAGCTTTT 2760
Db 2595 ATTGGGATCAATGACGTTTCTGCTTAAACCAAGCTACCAATCTTGTGAGCAAGCTTT 2654
Qy 2761 AGTCCTTCGTGAGGAAACCTTTTGTCTTAACTCAAAATTTGAGCCCTTTAGCCAAAT 2820
Db 2655 CATAGTTCCGGGGTAAACCATTTGCTTAACTCTGCTGTTGAGATGTTGAGTCAGT 2714
Qy 2821 TTCTTTTGAATTCGGTGTGCTATCTGCAATTTCAATTTAGACTTAGAGGCAAAATACCA 2880
Db 2715 TGGTTTCGAATTCAGAACTCTTCAAGAAATTTAAGCTAGATCTTGGGCTAAGGTCG 2774
Qy 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 6

US-10-312-273-96
; Sequence 96, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; PRIORITY FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 96
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-96

Query Match 17.6%; Score 527; DB 16; Length 2787;
Best Local Similarity 52.9%; Pred. No. 2.4e-118;
Matches 1413; Conservative 0; Mismatches 138; Indels 75; Gaps 10;
Qy 247 TGCTGGAATACCTACCTATTAAAGGAAATGTCTACTCTAGAAAATATTCTCTGGAACAGG 306
Db 156 TACTGGAATAGACTATATCTCTGACAGGAGATATAACTCTGCAAAACCTTGGGATTCGG- 214
Qy 307 CACGCAATCAAAAAAGCTGTTTAAACAACACTAAGGCGGATTTGACTTTTCAAGGTAA 366
Db 215 --CAGCTTAAAGGAGGTTGTTTCTGACACTACGGAATCTTTAAAGCTTTGCCGTAA 272
Qy 367 GGGGAATCTCTATTGTTCCAAAACGTTGATGACAGGACTGTAGCAGGGGCTGCTTAA 426
Db 273 GGGGTACTCACTTCTTTTAAATATTAAAGTCTAGTCTGAAAGCGCAGCACTTTCTGT 332
Qy 427 CAGCAGCGTGTAGATATAATCTACCAAGTTTATAGGGTTTCTTCGCTATCTTTTATTCG 486
Db 333 TACAACCTGATATAAATCTGTCTGCTAAAGGATTTTCGAGTCTTACTTTCTTAGCGGCC 392
Qy 487 GTCTCTCGAAGTTTCGATAAATCTACCGCAAGAGCGCGTTAGCTGTCTACCGGTAGCTT 546
Db 393 ATCATCGGTAAATCAACACCCCTCAGGAAAGGTCAGTTAAATGTGGAGGGGATC--T 449
Qy 547 GAGTTTGACAAAATATGTCAGTTTCTCTTCTGACGAAAACCTTTTCAACGATAATGCGCG 606
Db 450 TACATTTGATACAAATGGAATCTATTATTTAAACAAGATTTACTGTGAGGAAATGCGCG 509
Qy 607 TGCTATACCGCAAAACCTCTTTTCAATTAACAGGACTACAAATGTGAGCTCTGTTTCTGA 666
Db 510 AGCCATTTCTACCAAGATCTTTCTTGAACACAGCAGCGGATCGATTTCTTTTGAAGG 569
Qy 667 AAATA-----CCTCCTCAAGAAAGCGGAGCCATTCAGACTTCGAGTCCGATGCCCTTAC 717
Db 570 GAATAAATCGAGCGCAACAGGGAAGGTCGGGCTATTTCGTGCTACTGCTACTGTAGA 629
Qy 718 CATTTCTGGAACCAAGGGAGTCTCTTTTCTGACAAATCTTTCGATTTCTGGAGC 777
Db 630 TATTACAAATATACGGCTCTTACCCCTCTTCTCGAACAAATTTGCTGAAGCTGCAGTGG 689
Qy 778 TGCAATTTTACAGAAAGCTCGTCTGACTATTCTAATATGCTAAAGTTTCTCTTTATTGA 837
Db 690 AGCTATAATAGCAAGGAACTGTACAAATTAAGGAAATACGCTCTCTTTGATTTTCTGA 749
Qy 838 CAATAAGGTCAAGAGCGAGCTCTTCAACACAGGGGATATGTCAAGGAGTGTCTATCTG 897
Db 750 AAATAGTGTGAC---AGCGACCGCAGGAAATGGAGGAGCTCTTCTGAGAGATGCCG--- 802
Qy 898 TGCTTATAAAACTAGTACAGATACTAAGGTCAACCTCACTGGAAATCAGATGTTACTCTT 957
Db 803 -----ATGTTACCATATCTGGAAATCAGATGTAATCTT 836
Qy 958 CAGCAACAATACATCGACAAAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGTGGC 1017
Db 837 CTCAGGAACCAAGCTGTAGCTTAATGGCGGAGCAATTTATGCTAAGAGCTTACACTGGC 896
Qy 1018 TTCCGGAGGAC-----TTACCCCTATTCTAGTGAATAATGTCTCAATGAGAGTACAGTCC 1071
Db 897 TTCCGGGGGGGGGGGTATCTCTTTTCTAAACAATAATAGTCCAAAGTACCAGTGCAGG 956
Qy 1072 TAAAGGTGAGCCATAGCTATCGAAGATAGTGGGAAATTCAGTTTATCCCGGATAGTGG 1131
Db 957 TAAAGTGGAGCCATTTCTTATCTAGCAGCTGGAGAGTGTAGTCTTTTCAGCAGAAAGCAGG 1016
Qy 1132 TGACATTTGCTTTTAAAGGAATACAGTCACTTCTACTACTCC---TGGGACGAATAGAAG 1188
Db 1017 GGCATTTACTTCAATGGGAAATGCCAATTTGTGCAACTACACCAAACTACAAAAAGAAA 1076
Qy 1189 TAGTATCGACTTAGGAACAGAGTGCAGAGATGACAGCTTTGCGTTCTGCTCTGCTAGAGC 1248
Db 1077 TTCTATTGACATAGGATCTACTGCAAGATTCAGAAATTTACGTTGCAATATCTGGGCAATAG 1136
Qy 1249 CATCTACTTCTATGATCCCACTACTACAGATCATCCACAACAGATTACAGATGCTTTAAA 1308

1137 CATCTTTTCTACGATCCGATTAAGTCTGCTTAATACGCGCTGCGGATCTACAGATCTTTAAA 1196
1309 AGTTAATGAGACTCCGCGAGATCTGACATCAATATACAGGGAACATCATCTTCACAGG 1368
1197 TCTCAATAAGGCTGATCAGGATAATAGTACAGATTAATAGTGGGTCGATGTTTTCTGG 1256
1369 AGAAAGTTATCAGAGACAGAGCGCGAGATTCTTAAATAATCTTACTTCGAAGCTACTACA 1428
1257 TGAAGAATCTCTGAAGATGAAGCAAAAGTTGACAGACAACTCACTTCTACGCTGAAGCA 1316
1429 GCCTGTAATCTTTACGAGGATCTCTATCTTTTAAACATGAGAGTACTCTGCACTCA 1488
1317 GCCTGTAATCTTAACTCAGGAAATTTAGTACTTAAACGTTGCTCACTCTCGATACGAA 1376
1489 GGCATTCACTCAACAGACAGATCTCTCTCGAAATGAGAGTACTACTCTAGAAC 1548
1377 AGGCTTTACTCAGACCGCGGCTTCTCTGTTATTTAGTATGATGCGGCAACGTTTAAAGC 1436
1549 ---TGTGATACTAGCACCATAAACAATTTGGTCAATTAACAATCACTATAGACGCTGC 1605
1437 AAGTACAGAGAGTCACTTTAAGAGTCTTCAATTCCTGTAGACTCTTTAGCGAGGG 1496
1606 AAGAAGGCAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCAT 1665
1497 TAAGAAAGTTGTAATTTCTGCTCTGAGCAAGTAAATAATGTAGCCCTTAGTGCTCGAT 1556
1666 CACTTTATTGACCCGAGCGGCTTTTATGAAATCATAGTTTAAAGTCTCTAGTC 1725
1557 TCTTCTTTTGGATACCAAGGGAATGCTTTATGAAATCAGACTTTAGGAAAACTCAAGA 1616
1726 CTACGACATCTTAGAGCTCAAGGCTCTGGAACCTGTAAACAGCACCGCAGTCTCAGA 1785
1617 CTTTTCATTTGTCAGCTCTCTGCTGAGTACTGCAACAACTACAGATGTTCCAGCGGT 1676
1786 TCCATAATGGGTGAGAAATTCATATACGGCTATCAGGAACTTTGGGCCCCAATTTGTTG 1845
1677 TCCTACAGTAGCAACTCTCAGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGT 1736
1846 GG-----GGACAGGGCTTCTACGACTGCAACCTTCACTGGACTTAAACTGG 1893
1737 TGATGATACCGCAAGCACTCAAAGACTAAGACAGCAGACATAGCTTGGACCAATACAGG 1796
1894 CTATATTCTTAATCCGAGGATCTGCGCTCTTTAGTCCCTAATAGCTTATGGAATGCAAT 1953
1797 CTACCTTCGAATCTTGAGGCTCAAGGACCTTTAGTTCCTAATAGCTTTGGGATCTTT 1856
1954 TATAGATATAGCTCTCTCAATATCTTATGGAGACTGCAACAGAGGTTGAGGAGGA 2013
1857 TCCAGACATCCAAAGCGATTCAAGGTGTCTATAGAGAGAGTGTCTTGAATCTTTGTTTCA 1916
2014 CCGTGTCTTTTGGTGTGCTGATATCTAATCTTCTCCATAAGGATAGTACAAACACG 2073
1917 TCGAGGCTTCTGGGCTGCGGAGTCCGCAATTTCTTAGATAAAGATAAGAAAGGGGAAA 1976
2074 ACGCGGTTTTCGCCATTTAGTGGCGGTATGTCATAGAGAGGAAACCTACATATCTTTTC 2133
1977 ACCCAATACCGTCATAAATCTGGTGAATGCTATCGGAGGTGACGCGCAACTTTGTTTC 2036
2134 AGATAAGATCTTAGTGTGCTGATTTTGTGAGCTCTTTGGAAGAGATAGAGACTTTTGT 2193
2037 TGAAGAACTTAATAGCTTTGCGCTTTTGCCAACTCTTTGGTGGGATAAAGATTTCTTAGT 2096
2194 AGCTAAGATCAAGGTACAGTCTACGAGGAACTCTCTATTACAGCAGCAACGAACCTTA 2253
2097 CGCTAATAATCACTGATACCTATGACGAGGCTTCTATATCAACAACTTACAGAAATG 2156
2254 TATCTCTCTCTTCGAAACTACGCGCTTGTGCTGTCTTATGTTCTCTACAGAGATTC 2313
2157 TAGTGGGTTTCATAGTTGTCTCTTAGATAAA---CTTCTGGCTCTTGGAGTCATAAAC 2213
2314 TGTCTCTTTTCAGGAACTTACCTAGCTACACCCATACGGAATACGATCTGAAACCAAGTA 2373

2214 CCTGGTTTTAGAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTA 2273
2374 TACAACATATCTCTACTGTTTAAAGAAAGCTGGGGAAATGATAGTTTCGCTTTTGAATTCGG 2433
2274 TACTGCGTATCTCTGAGGTGAAGGTTCTTGGGGGAATAATGCTTTTAAACATGATGTTGGG 2333
2434 TGAAGAGCTCCGATTTGCTTAGATGAAGTGCTCTATTTTGGAGCAGTACATGCCCTTCAT 2493
2334 AGCTTCTTCAATCTTATCTGTAATACCTGCAATGTTTGTATACCTATGCTCCATACAT 2393
2494 GAAATTCGAGTTTGTCTATGCACATCAGGAAGGTTTTTAAAGAAACAGGAAGCTCG 2553
2394 CAAACTGAATCTGACCTATATAGCTCAGGACAGCTTCTCGAGAGAAAGTACAGAGGAAG 2453
2554 TGAATTTGGAGTAGCCGCTCTTGTGAATCTTGCCTTACCTATCGGATTCGATTTGTATA 2613
2454 ATCTTTTGTATGACAGCAACCTCTTCAATTTATCTTGCCTATAGGGGTGAAGTTTGAGAA 2513
2614 GGAATCAGACTGCCAAGATCAACGTACAATCTTAACCTTTGTTTATCTGTGATCTTGT 2673
2514 GTTCTCTGATGTAAAGACTTTTCTTATGATCTGACTTTATCCTATGTTCTCTGATCTTAT 2573
2674 TCGTAGTAACCCGACTGTACGACAACTCGCAATTTAGCGGTGATTTCTTTGAAAACTT 2733
2574 CCGCAATGATCCCAATGCACTACAGCACTTGTAAATCAGCGAGCCCTTTGGGAACTTA 2633
2734 CGGTACGAATTTGGCAAGACAAAGCTTTAGTCTTCTGTCGAGGGAACCAATTTTGTCTTAA 2793
2634 TGCAATTAATTTAGCAGCAGAGCCCTTGCAGTGCCTGAGGAGTCACTACGCTTCTC 2693
2794 CTCAAATTTTGAAGCCCTTTAGCCAAATTTTCTTTTGAATTCGCTGGGTCACTCTCGCAATTA 2853
2694 TCTATGTTTGAAGTGTCTGCGCCAGTTGCTTTTGAAGTTTCGTTGATCTTCAAGGATTA 2753
2854 CAATGTAGACTTAGGAGCAAAATACCAATTTCTA 2886
2754 TAATGTAGATCTTTGGGGTAAAGTTCCAAATTTCTA 2786

RESULT 7

US-10-312-273-18
; Sequence 18, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 18
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-18

Query Match		17.4%; Score 523; DB 16; Length 534;	
Best Local Similarity		99.8%; Pred. No. 1e-137;	
Matches 534; Conservative		0; Mismatches 0; Indels 1; Gaps 1;	
QY	101	ATGAAGTCTCTTTCCCAAGTTTGATTTCTACATTTGCTATTTTCCCTTTGCTATG	160
DB	1	ATGAAGTCTCTTTCCCAAGTTTGATTTCTACATTTGCTATTTTCCCTTTGCTATG	60
QY	161	ATTGCTACGACAGATTTTGATTTCAAGTGGCGATTTTCGATGGGAATATAAATGGTAAT	220
DB	61	ATTGCTACGACAGATTTTGATTTCAAGTGGCGATTTTCGATGGGAATATAAATGGTAAT	120
QY	221	TTTTTCAGTTTCGAGAGTCAGGAAGATGCTGGAACTACTACCTATTTTAAGGGAAATGTC	280
DB	121	TTTTTCAGTTTCGAGAGTCAGGAAGATGCTGGAACTACTACCTATTTTAAGGGAAATGTC	180
QY	281	ACTCTAGAAAATATTTCTGGAAACAGGACAGCAATACAAAAAGCTGTTTAAACAACAT	340
DB	181	ACTCTAGAAAATATTTCTGGAAACAGGACAGCAATACAAAAAGCTGTTTAAACAACAT	240
QY	341	AAGGGCGATTTGACATTTACAGGTAACGGAACTCTCTATTGTTCCAAACGGTGGATGCA	400
DB	241	AAGGGCGATTTGACATTTACAGGTAACGGAACTCTCTATTGTTCCAAACGGTGGATGCA	300
QY	401	GGGACTGTAGCAGGGGCTGCTCTTAACAGCAGCGTGGTAGATAAATCTACACAGTTTATA	460
DB	301	GGGACTGTAGCAGGGGCTGCTCTTAACAGCAGCGTGGTAGATAAATCTACACAGTTTATA	360
QY	461	GGGTTTTCTTCGCTATCTTTTATTTGCGTCTCTCGAAGTTCGATAACTACCGGCAAGGA	520
DB	361	GGGTTTTCTTCGCTATCTTTTATTTGCGTCTCTCGAAGTTCGATAACTACCGGCAAGGA	420
QY	521	GGCGTTAGCTGCTACGAGGTAGCTTGAGTTTGACAAAAAATGTCAGTTTCTCTCAGC	580
DB	421	GGCGTTAGCTGCTACGAGGTAGCTTGAGTTTGACAAAAAATGTCAGTTTCTCTCAGC	479
QY	581	AAAAAATTTTCAACGGATTAATGGCGTGTCTATCACCGCAAAAAATCTTTTCATTAA	635
DB	480	AAAAAATTTTCAACGGATTAATGGCGTGTCTATCACCGCAAAAAATCTTTTCATTAA	534
RESULT 8			
US-10-312-273-34			
; Sequence 34, Application US/10312273			
; Publication No. US20040005667A1			
; GENERAL INFORMATION:			
; APPLICANT: CHIRON SA			
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE			
; FILE REFERENCE: P025035WO			
; CURRENT APPLICATION NUMBER: US/10/312,273			
; CURRENT FILING DATE: 2002-12-20			
; PRIOR APPLICATION NUMBER: 0016363.4			
; PRIOR FILING DATE: 2000-07-03			
; PRIOR APPLICATION NUMBER: 0017047.2			
; PRIOR FILING DATE: 2000-07-11			
; PRIOR APPLICATION NUMBER: 0017983.8			
; PRIOR FILING DATE: 2000-07-21			
; PRIOR APPLICATION NUMBER: 0019368.0			
; PRIOR FILING DATE: 2000-08-07			
; PRIOR APPLICATION NUMBER: 0020440.4			
; PRIOR FILING DATE: 2000-08-18			
; PRIOR APPLICATION NUMBER: 0022583.9			
; PRIOR FILING DATE: 2000-09-14			
; PRIOR APPLICATION NUMBER: 0027549.5			
; PRIOR FILING DATE: 2000-11-10			
; PRIOR APPLICATION NUMBER: 0031706.5			
; PRIOR FILING DATE: 2000-12-22			
; NUMBER OF SEQ ID NOS: 664			
; SOFTWARE: SeqWin99, version 1.02			
; SEQ ID NO 34			
; LENGTH: 2787			
; TYPE: DNA			
; ORGANISM: Chlamydia pneumoniae			

1251 TCTACTTCTATGATCCATAAAGTACAGATCATCCACAAGTTTACAGATGTTCTTAAAG 1310
1142 TCTACTTCTATGATCTTAAACAACTAGCATCACTGAGCTCTCTAGATGCTCTAACT 1201
1311 TTAATGAGACTCCGGCAGATTTCTGCATCAATATACAGGAAACATCATCTTACAGGAG 1370
1202 TAAATGGTCTGACCTTGACGGAATCCTGCATATCAAGGAACCATCGTATTTCTGAG 1261
1371 AAAAGTTATCAGAGACAGAGCGCAGATTTCTAAATCTTACTTCTGAACTACTACAGC 1430
1262 AGAAGCTCTCGAAGCAGAGAGCTGCAGAGCTGATTAATCTCAAATCTACAAITTCAGCAAC 1321
1431 CTGTAACTCTTTTTCAGGAGTACTCTATCTTTTAAACATGAGTACTCTCGAGACTCAGG 1490
1322 CTCTAACTTTTGGGAGGCACTCTCTCTTAAATCAGAGTCACTCTCTAGTTGCTAAGT 1381
1491 CATCTACTCAACAGGCGAGATTTCTGCTCGAAATGGACGTAGGAATCTCTAGAACCTTG 1550
1382 CTTTTTCGCAATCTCGGGCTCTACCTCTCTCTGATGTCAGGACCCACATTTAGAAACCG 1441
1551 CTGATCTAGCACCATAAACAAATTTGGTCAATTAACATCACTTCTATAGACGTTGCAAGA 1610
1442 CTGATGGATCACTATCAATAATCTGTTCTCAATGTAGATTCCTTAAAGAGACCAAGA 1501
1611 AGGCAAAATAGAAACCAAGCTACGTCAAAATCTGACTTTATCTGGAAACCATCACTT 1670
1502 AGGCTACGCTAAAGCAACACAGCAAGTCAGACAGTCACCTTTATCTGGATCGCTCTCTC 1561
1671 TATTGACCGCAGCGGACGCTTTTATGAAATCATAGTTTAAAGAAATCTCTAGTCTTACG 1730
1562 TTGTAGATCTTTCTGGAATGTCTAGCAAGTGTCTCTTGAATGCTCTTGAATCAAGCTTTT 1621
1731 ACATCTTAGAGCTCAAGCTT-----CTGGAATGTAAACAGCAGCTACTCCAG 1784
1622 CTGTCTCACTCTTACTGCTGACGACCCCGCAATATTCACATCAACAGATTTAGCTGCTG 1681
1785 ATCCTTAATATGGGTGAGAAATTCATTTACGGCTATCAGGGAACTTGGGGCCCAATTTT 1844
1682 ATCCCTAGAAATATCCTATCCATTTGGGATACAGGGAAATGGGCAATTTCTTGGC 1741
1845 GGGGACAGGGC-----TTTACGATCGCAACCTTCAACTGAGCTAAACCTGGCTATA 1898
1742 AAGAGGATACGCGACTAAATCCAAAGCAGCGACTCTTACCTGGACAAAACAGGATACA 1801
1899 TTCTTAATCCGAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGAAATGCAATTTATAG 1958
1802 ATCCGAATCTGAGCGTGGGAACTTGTGCTAACACGCTATGGGGATCCTTTGTTG 1861
1959 ATATTAGCTCTCTCCATTTATTTATGGAGACTGCAAAACGAAGGTTGCGAGGAGACGGTG 2018
1862 ATGTGCGCTCCATACACAGCTTTGTAGCCACTAAAGTACGCCAATCTCAAGAACTCGCG 1921
2019 CTTTTTGGTGTGCTGATTAATCTAACTTTTCCATAGGATAGTACAAAACAGCAGCG 2078
1922 GCATCTGGTGTGAAGGATCTCGAATCTTCTTCCATAAAGATAGCAGCAAGATAAATAAG 1981
2079 GTTTTCCGCAATTTAGTGGCGTTATGTCATAGAGGAACCTACATCTTTGTCAGATA 2138
1982 GTTTTTCCGCAATAGTGGAGGTTATGTTGTAGAGGCACTACAACATTAGCTTCTGATA 2041
2139 AGATTTCTTAGTGTGCTATTTGTGCTGCTTTTGGAAAGATAGAGACTCTTTGTAGCTA 2198
2042 ATCTTATCACTGAGCTTCTGCCAATTTATCGGAAAGATAGAGATCACTTTTAAATA 2101
2199 AGAATCAAGTACAGTCTACGAGGAACTCTCTTATTAACGACCAAGCAACCTATATCT 2258
2102 AAAATAGAGCTTCTGCTATGAGCTTCTCTCCATCTCCAGCATCTAGCAGCTTGTCTT 2161
2259 CTCTTCTTCAAACTACGCGCTTGTGCTGTTCTTATGTTCTTCTACAGAAATCTCTGTT 2318
2162 CTCGAAAGCTTGTAC-----GCTACCTTCTGATCTGAAAGTGAAGCAGCCTGTCC 2212

2319 TCTTTTCAGAAACCTTAGCTACACCATACGATAACGATCTGAAACCAAGTATACAA 2378
2213 TCTTTGATGCTCAGATCAGCTATATCTATAGTAAAATACTATGAAACCTATTACACCC 2272
2379 CATATCTTACTGTTTAAAGGAAGCTGGGGGAATGATAGTTTCGTTTGAATTCG--GTG 2435
2273 AAGCACAAAGGAGAGAGCTCGTGTGATTAATACGCGTTGCGCTCTGGAACCTTGCAGCT 2332
2436 GAAGAGCTCCGATTTGCTTAGATGAAGTCTCTATTTAGAGCAGTACATGCCCTTCAATGA 2495
2333 CCTTACACACACTGTTTTAAGCCATGAGGCTCTCTTCCACGCGTATTTTCTTTTCATCA 2392
2496 AATGCGAGTTTGTCTATGCACATCAGAAAGGTTTTAAAGAAC--AGGGAACAGAAAGCTC 2552
2393 AAGTAGAGCTTCGTATACATACCAAGATAGCTTCAAAGAACGTAATACTTACCTTGGTAC 2452
2553 GTGAATTTGGAAGTAGCGGCTTTGTGAATCTTCCCTTACCTATCGGATCCGATTTGATA 2612
2453 GATCTTTTCGATAGCGGTGATTTAATTAACGCTCTCTGTGCCCTATTGGAATTACCTTCGAGA 2512
2613 AGGAATCAGACTGCCAAGATGCAACGTACAACTTAACCTCTGTTTATCTGTTGATCTTG 2672
2513 GATCTCGAAGAACGAGCGTGTCTTTACGAAGCTACTGTCATCTAGTTGCCGATGTCT 2572
2673 TTCTAGTAAACCCGACTGTACGACCAACTGCGAATTTAGCGGTGATTTCTTGAAACCT 2732
2573 ATGTAAGATCTGACTGCACGACAGCTCTCTAATCAACATACCTCGTGAAACTA 2632
2733 TCGGTAAGATTTGGCAAGACAGCTTTAGTCTCTCGTGAGGGAACCAATTTTGTCTTTA 2792
2633 CAGGAACGAATCTCTCAAGACAGCTGGTATCGAAGAGCAGGGATCTTTTATGCTCTCT 2692
2793 ACTCAATTTGAGCCTTTAGCCAATTTCTTTTGAATTTGCGTGGTGTATCTCGGAAT 2852
2693 CTCCAATCTTGAAGTCAACAAGTAACTATCTATGGAATTCGTGGATCTTCAAGCAGCT 2752
2853 ACAATCTAGACTTTAGGAGCAAAATACAAATCTCAA 2887
2753 ACATCGACATCTTGGAGGTAGTTCCAGTTCTAA 2787

RESULT 9

US-10-282-122A-18496
; Sequence 18496, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578

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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18496
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-18496

Query Match          17.1%; Score 514; DB 13; Length 2793;
Best Local Similarity 52.7%; Pred. No. 1.2e-134;
Matches 1404; Conservative 0; Mismatches 1200; Indels 60; Gaps 11;

QY 250 TGGAACTACCTATTTAAGGGAATGTCACTCTAGAAATATTCCTGGACAGGCAC 309
DB 162 TGGAACTACCTATTTAAGGGAATGTCACTCTAGAAATATTCCTGGACAGGCAC 218
QY 310 AGCAATCAAAAAGCTGTTTTAAACAACATAAGGCGGATTTGACTTTACACAGGTAACGG 369
DB 219 AGCAATCAAGGCTGCTTTACAGAACTACGGGTGATCTGACATTTACTTGGAAAGGG 278
QY 370 GAACCTCTATTGTTCCAAACGGTGGATGACAGGGACTGTAGCAGGGGCTGCTGTTAAACAG 429
DB 279 ATACTCAATTTCAATCAACAGGTAGATGCGGGTTGCAATGACAGGAGCTGCGG---CAAG 335
QY 430 CAGCGTGGTAGAATAATCTACACGTTTATAGGTTTCTTCGCTATCTTTTATTGCGTC 489
DB 336 CAAACTGCTGATAAGCCCTTAACATTCACAGGATTTTCTAACCTTTCTTCAATGACGC 395
QY 490 TCTCGAAGTTCGATAACTACCGGAAAGGCGGTAGCTGCTCTACGGGTAGCTTGAG 549
DB 396 TCTCGAAGTTCGATAACTACCGGAAAGGCGGTAGCTGCTCTACGGGTAGCTTGAG 452
QY 550 TTGCAAAAATAGTCAGTTTCTCTTACGCAAAAATTTTCAACGG-----ATAA 600
DB 453 TCTTACCGAATAATGGAAGATTTCTTTAGCAAAAACGCTCTCAATGAAGCTAATAACAA 512
QY 601 TGGCGGTGCTATCACGCAAAAACCTTTTCATTAACAGGACTACAAATGTCAGCTCTGTT 560
DB 513 TGGCGGAGGATCACCAAAAACCTTTTCTATTTCTGGGAATACCTCTTCTATTAACCTT 572
QY 661 TTCTGAAATACCTCTCTCAAGAAAGGCGGAGCAATTCAGACTTCCGATGCCCTTACCAT 720
DB 573 CACTAGTAATAGCGCAAAAATTTAGGTGGAGGATCTATAGCTCTGCGGCTGCAAGTAT 632
QY 721 TACTGAAACCAAGGGAAGTCTCTTTTCTGCAATATCTTCTTGGATCTTGGAGCTGC 780
DB 633 TTCAAGAAACACGGGCACTTGTATGTAATATAAAGGAGAACTGGGGGTGGGGC 692
QY 781 AATTTTTACAGAGCTCGGTGACTATTTCTAATATGCTAAAGTTTCTTTTATTGACAA 840
DB 693 TCTGGGCTTTGAAGCAGCTCTCTGATTTACTCAAAATAGCTCCCTTTCTCTGGAATA 752
QY 841 TAAGGTACAGGAGGAGCTCTCTCAACACGGGGGATATGTACAGGAGGTGCTATCTGTGC 900
DB 753 CACTGCAACAGATGCTGCAGGCAAG-----GGCGGGGCCATTTATTG 794
QY 901 TTATAAACTAGTACAGATCTAAGGTCAACCTCACTGGAATCAGATGTTACTCTTACAG 960
DB 795 TGAATAAAACAGGAGAGACTCTACTCTTACTATCTCTGGAAATAAAGTCTGACCTTCGC 854
QY 961 CAACTATACATCGACAAACAGCGGAGGAGCTATCTATGTAAGAAAGCTCGAACTGGCTTC 1020
DB 855 CGAAACTCTTCTAGTAACCTCAAGGCGAGCAATCTGTGCCATGGTCTAGATCTTCCGC 914

1021 CGGAGGACTTACCCCTATTTCAGTAGAAATAGTGTCAATGAGGTACAGCTTCTTAAAGGTGG 1080
DB 915 TGCTGGCCCTACCCCTATTTCCTAAATAATAGATGCGGGAACACAGCTGCGAGGCAAGGGCG 974
QY 1081 AGCCATAGCTATCGAAGATAGTGGGGAATGAGTTTATCCGCCGATAGTGGTACATGTT 1140
DB 975 CGCTATTGCAATTTGCCGACTCTGGATCTTTAAGTCTCTCTGCAAAATCAAGGAGACATCAC 1034
QY 1141 CTTTTTAGGGAATACAGTCACTTCTA---CTACTCTCGGAGCAATAGAAAGTAGTATCGA 1197
DB 1035 GTTCTTGGACACTCTTAACCTCAACCTCGCGCAACATCGACACGGAATGCTATCTA 1094
QY 1198 CTTAGGAACGAGTGCAGAGATGACAGCTTTTGGCTTCTGCTGCTGTAGAGCCATCTACTT 1257
DB 1095 CCTGGATCGTCCAGCAAAAATTTACGAATTAAGGCGAGCCCAAGGCCAATCTATCTATT 1154
QY 1258 CTATGATCCCTAATACAGGATCATCCACAACAGTTACAGATGTTCTTAAAGTTAATGA 1317
DB 1155 CTATGATCCGAT---TGCATCTTAACACACAGGAGCTTCAGACGTTCTGACCATCAACCA 1211
QY 1318 GACTCCGCGAGATTTCTGCACTACAATATACAGGGAACATCATCTTTCACAGGAGAAAGTT 1377
DB 1212 ACCGATAGCACTCGCTTTAGATTATTAGAAAGATTTGATTTTCTGGGAAAGCT 1271
QY 1378 ATCAGAGACAGAGCGCGCAGATTTCTAAAAATCTTACTTCGAAAGCTACTACAGCTGTAA 1437
DB 1272 CTCTCAGATGAAGCAAGCTGCTGATAAATCTTCACTCTATTTAAAGCAACCATTTGC 1331
QY 1438 TCTTTACAGAGTACTCTATCTTTTAAACATGAGAGTGACTCTGCGACTCAGGCAATTCAC 1497
DB 1332 TCTAGCTCTTGGAACTTAGCACTCAAGGAAATCTCGAGTTAGATGTCAATGGTTTTCAC 1391
QY 1498 TCAACAGGCGAGATTTCTGCTCTGAAATGAGCGTAGGAATCACTCT---AGAACTCTCTGA 1554
DB 1392 ACAGACTGAAGCTCTACACTCTCATGCAACCAAGCAAGCTCAAGAGATCTGA 1451
QY 1555 TACTAGCAACCAATTAATTTGGTCAATTAACATCAGTTCTATAGACGGTGCAGAAAGGC 1614
DB 1452 AGCTATCAGTCTTACCAAACTTGTGTTGATCTTTCTGCTTAGAGGGAATAAGAGTGT 1511
QY 1615 AAAAATAGAACCAAGCTACGTCAAAATCTGCTTTTATCTGGAACCATCACTTTAT 1674
DB 1512 GTCCATTAAGACAGGAGGAGCAACAAACTATACTCTCTCTCTCTCTCTCTCTCTCTCT 1571
QY 1675 GGACCGGAGCGGCTTTTATGAAAAATCATAGTTTAAAGAAATCTCTCAGTCTCTACGACAT 1734
DB 1572 AGATAGTAGCGCAATTTTATGAAGCAATACGATAAACCAAGCTTTCAGCAGCTTT 1631
QY 1735 CTTAGAGCTCAAGGCTCTGGAACCTG-----TAAACAGACCGCAGTGACTCCAGA 1785
DB 1632 GGTGGTATTCTGCTGCTACTGCTAGCGATATTTATATCGATGCGCTTCTCACTTC 1691
QY 1786 TCTTATTAATGGGTGAGAAATTCCTATCGGCTATCAGGAACTTGGGGCCCAATGTTTG 1845
DB 1692 TCCAGTACAACTCCAGAACCTCATTCAGGGTATCAGGACATTTGGAAAGCACTTGGGC 1751
QY 1846 GGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGAATAAACTGGGTATATTTCTCTAA 1905
DB 1752 AGACATCACTGCAAAATCAGGAATATGACTTTGGGTAACTACGGGCTACAAACCTAA 1811
QY 1906 TCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTTATGGAATGCAATTTATAGATTTAG 1965
DB 1812 TCTGAGCGTAGAGCTTCGTTAGTTCCCGATTCATTTATGGGCATCTTTTACTGACATTCG 1871
QY 1966 CTCTCTCAATATCTTATGAGACTGCAAAACGAAGGTTGAGGAGAGACCGTCTTTTGG 2025
DB 1872 CACTCTACAGAGATCATGACATCTCAGCGAATAGTATCTATCAGCAAGGAGACTCTG 1931
QY 2026 GTGTGCTGATTATCTAACTTCTTCCATAAGGATAGTACAAAACACGACGCGGTTTCG 2085
DB 1932 GGCAATCAGGAACCTGCGAATTTCTTCCATAAGGATTAATCAGGAACCTAAACCAAGCATTCG 1991
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QY 2086 CCATTGAGTGGCGGTATGTATGATAGGAGGAAACCTACATCTTGTTCAGATAAGATTCT 2145
Db 1992 ACATAAAGCTACGGCTATATTTGGAGGAAGTGCTGAAGATTTTCTGAAATATCTT 2051
QY 2146 TAGTGTGCATTTTGTGAGCTTTTGAAGAGATAGAGATCTTTGTAGCTAAGATCA 2205
Db 2052 CAGTGTAGCTTTTGGCAGCTCTTCGCTAAAGATAAAGACCTGTTTATAGTTGAAATAC 2111
QY 2206 AGGTACAGTCTACGAGGAACTCTCTATTACACGACACAAAGAAACCTATATCTCTCTCC 2265
Db 2112 CTCTCATAACTATTAGCGTGCCTATACCTGCAACATCGAGCATCTCTAGAGAGACTTCC 2171
QY 2266 TTGCAAACTACGGCTTTGTTGTTGTTTCTTATGTTCTTACAGAGATCTCTGTTCTTTTC 2325
Db 2172 ---CATGCCCTCATTTGGAAGTATCACCGACATGCTGAAAGATATCTCTCATTTTGAA 2228
QY 2326 AGGAAACCTTAGCTACACCCATACGGATACGATCTGAAACACCAAGTATACACATATCC 2385
Db 2229 TGCCAGCTAAGCTACAGCTACACTAAATAATGATATGATACCTCGCTATATCTCTATCC 2288
QY 2386 TACTGTTTAAAGGAAGCTGGGGGAATGATGTTTTCGCTTTAGATTCGGTGA---AGAGC 2442
Db 2289 TGAAGCTCAGGCTCTTGGACCAATAACTCTGGGGCTCTAGAGCTCGAGGATCTCTGGC 2348
QY 2443 TCCGATTTGCTTAGATGAAAGTGTCTTATTTGAGCAGTACATGCGCTTCATGAAATTGCA 2502
Db 2349 TCTATATCTCCCTAAAGAACACCGTCTCTCCAGGGATATTTCCCTTCTTAAAGTTCCA 2408
QY 2503 GTTGTGCTATGCACATCAGAGAGTTTAAAGAACAGGGAACAGAGCTCTGTGAATTTGG 2562
Db 2409 GGCAGTCTACAGCGGCCAACAAACCTTAAAGAGAGTGGCGCTGAAGCCGCTGCTTTTGA 2468
QY 2563 AAGTAGCGCTTGTGTAATCTTGCTTTACCTATCGGGATCCGATTTTCATAGGAATCAGA 2622
Db 2469 TGAATGAGAGCTTAGTGAACCTGCTCTATCTCTGCGGATTCGGTTAGAAAAATCTCCGA 2528
QY 2623 CTGCCAAGTGCACGTPACAACTPAACCTCTGTGTTATACCTGTGATCTTGTTCGTAGTAA 2682
Db 2529 AGATGAAAAAATAATTTTCAGATTTCTCTAGCCTACATTTGTGTATGTTATCGTAAAA 2588
QY 2683 CCCGACTGTACACACACATCGGAATAGCGGTGATCTTGGAAACCTCTCGGTAGCAA 2742
Db 2589 TCCCCGTTCGCTGACTTCTCTAATGCTCAGTGAGCCTCTTGGACTTTGCTATGTAATAAA 2648
QY 2743 TTTGGCAAGCAAGCTTTAGTCTCTCTGTCAGGGAACATTTTGTCTTAACTCAATTT 2802
Db 2649 CCTCGACGACAGCTTTCTAGCAAGTCTGGAAGCCATCTGACTCTCTCCCTCATGT 2708
QY 2803 TGAAGCCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTCTATCTCGCAATTACAAATGAGA 2862
Db 2709 AGAACTCTCGGGAAGCTGCTTATGAGCTTCGTGGCTCAGCACATCTACAAATGAGA 2768
QY 2863 CTTAGAGCAAAATACCAATTCTA 2886
Db 2769 TTGTGGCTAAGATACTCATTTCTA 2792
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RESULT 10

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US-10-312-273-46
; Sequence 46, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
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; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 46
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-10-312-273-46

Query Match 17.1%; Score 514; DB 16; Length 2793;
Best Local Similarity 52.7%; Pred. No. 1.2e-134;
Matches 1404; Conservative 0; Mismatches 1200; Indels 60; Gaps 11;

QY 250 TGAACCTACCTACCTATTTAAGGAAATGTCACCTCTAGAAAAATATTCCTGGAAACAGGCAC 309
Db 162 TGAACGAACCTATGCTTTATCAGGAATGCTATATAACGA---TGCTGGAAAGGCAC 218
QY 310 AGCAATCAGAAAAAGCTGTTTAAACACACTAAGGCGCATTTGACTTTCACAGTAACGG 369
Db 219 AGCATTAAACAGGCTGCTGCTTTTACAGAACTACGGGTGATCTGCATTTACTTGGAAAGG 278
QY 370 GAATCTCTATTTCTCCAAACGGTGGATCAGGAGCTGTAGCAGGGGCTCTGTTAACAG 429
Db 279 ATACTCATTTTCATTCACACGGTAGTCGGGTTCGAATGACAGAGCTCGGG---CAAG 335
QY 430 CAGCGTGTAGATAAATCTACACACGTTTATPAGGGTTTTCTTCGTATCTTTTATTTGCGTC 489
Db 336 CACAACCTGCTGATAAAGCCCTAACATTCACAGATTTTCTAACCTTTTCTTCTTATTCGAGC 395
QY 490 TCTGTGAGTTTCATTAACCTACCGGAAAGAGCGGTAGCTGTCTACGGGTAGCTTGAG 549
Db 396 TCTGTGAACTACAGTTGCTTTCAGAAAAAGTACTTTAA---GTTCTGACGAGGCTTTAAA 452
QY 550 TTTGACAAAAATGTCAGTTTGTCTTTCAGCAAAAACTTTTCAACGG-----ATAA 600
Db 453 TCTTACCGATAATGGAACGATCTCTTTAGCCAAAACGCTCCAAATGAAGCTAATAACAA 512
QY 601 TGGCGGTGCTATCACCGCAAAAACTCTTTTCATTAACAGGAGCTACAAATGTCTGTT 660
Db 513 TGGCGGAGCGATCACCACAAAAACTCTTCTATTTCTGGAATACCTCTTCTATACCTT 572
QY 661 TTTGAAAAATACCTCTCTCAAGAAAGCGGAGCGCATTCAGACTTTCGATGCCCTTACCAT 720
Db 573 CACTAGTAATAGCGCAAAAAAATTAGGTGAGCGATCTATAGCTCTGCGGCTGCAAGTAT 632
QY 721 TACTGAAAAACCAAGGGGAAGTCTCTTTTCTGACAATACTCTTTCGGATTTCTCGAGTCG 780
Db 633 TTCAGAAACACCGGCGCAGTTAGTCTTTATGATAATAAAGAGAAACCTGGGGGTGGGGC 692
QY 781 AATTTTTACAGAAAGCCTCGGTGACTATTTCTAATAATGCTTAAAGTTTTCTTTTATGACAA 840
Db 693 TCTGGGCTTTGGAAGCCAGCTCCTCGATTACTCAAAATAGTCCCTTTTCTTCTCTGAAA 752
QY 841 TAAGGTACAGGAGCGAGCTCCTCAACAAACGGGGGATATGTACAGGAGGTCTATCTGTGC 900
Db 753 CACTGCAACAGATGCTGACGGCAAG-----GGCGGGGCCATTATTG 794
QY 901 TTATAAACTAGTACAGATTAAGTCACTCACTGGAATCAGATGTACTCTTCAG 960
Db 795 TGAAAAAACAGGAGAGACTCTCTACTTCTCTGAAATAAAAAAGTCTGACCTTCGC 854
QY 961 CAACATATACGACAAACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGCTTC 1020
Db 855 CGAGAACTCTTCAGTAACTCAAGCGGAGCAATCTGTGCCATGGTCTAGATCTTTCGC 914
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QY 1021 CGAGGACTTACCTTAATCAGTAGAAATAGTGTCAATGGAGTACAGCTCCTTAAAGGTGG 1080
DB 915 TGCTGGCCCTACCCCTAATTTCAATAATAGATGCGGAACACAGCTGCGAGGCAAGGCGG 974
QY 1081 AGCCATAGCTATCGAAGATAGTGGGAATTAGTATTATCCGCCGATAGTGGTACATTTGT 1140
DB 975 CGCTATTGCAATTCGCGACTCTGGATCTTTAAGTCTCTCTGCAATCAAGGAGACATCAC 1034
QY 1141 CTTTATGGGAATACAGTCACCTCTA---CTACTCCTGGAGCAATAGAGTAGTATCGA 1197
DB 1035 GTTCTTGGCAACACTCTAACTCAACCTCCGCGCAACATCGACACGGAATGCTATCTA 1094
QY 1198 CTTAGGAACGAGTGCAGAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCCATCTACTT 1257
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RESULT 11

US-10-289-762-1/c

; Sequence 1. Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Grifais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1

; LENGTH: 1230025

; TYPE: DNA

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QY	1187	AGTAGTATCGACTTAGGAACGAGT	GCAAGATGACAGCTTGGGTTCT	CGTCTCGGTAGA	1246
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US-09-452-380-1
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; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: WANG, Joe
; APPLICANT: DUNN, Pamela
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE REFERENCE: 032931/0216
; CURRENT APPLICATION NUMBER: US/09/452,380
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
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; NUMBER OF SEQ ID NOS: 6
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US-09-452-380-1

Query Match 16.9%; Score 506.6; DB 9; Length 3050;
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QY	2076	CGCGGTTTCGCCAATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATCTGTTTCAG	2135
Db	2082	ATGTTTTCGCCATATCAGCGGGGTTATGCACCTAGGGATCAGAGCAACAACCTCTGCCG	2141
QY	2136	ATAGATTTCTTAGTGCTGCAATTTGTGACGCTCTTTTGGAGAGATAGAGACTACTTTGTAG	2195
Db	2142	AGGATCAGCTTACTTTTTCGCTCTCCAGACTCTTTGTCTAGAGATTCGCAATCATATTACAG	2201
QY	2196	CTAGAATCAAGGTACAGTCTACGGAGGAATCTCTATTACCAGC-----	2240
Db	2202	GTAAGAACCGAGGATACTTACGTGCTCTTTGTATTTCCACCATACAGAAGGCTCT	2261
QY	2241	---ACAAAGAAACCTATATCTCTTCCCTTGCRAACTACGCGCTTGTTCGTTGTCTTANG	2297
Db	2262	TCGACATCGCCAAATTCCTCTCGGGGAAAAGCAACCGAGCTCCCTGGGTGCTCTCTGAGA	2321
QY	2298	TTCTTACAGAGATTCCTGTCTCTTTTCAGGAACCTTAGCTACACCCATACGGATAACG	2357
Db	2322	TCTCCCAGATCATCTCTTATCGTTCGATGCTAAATTCAGTTATCTCCATACAGACAACC	2381
QY	2358	ATCTGAAAAACAGTATACAAATATCCTACTGTTTAAAGGAAGCTGGGGGAATGATAGTT	2417
Db	2382	ACATGAGACATATTATACCGATACTCTATCATCAAGGGTTCCTTGGAGAAACGATGCGCT	2441
QY	2418	TCGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTTAGATGAAGTGCTCTATTGAGC	2477
Db	2442	TCTGTGCAGATCTTGGAGCTAGCTGCTCTTTTGTATTTCCGTTTCCGTAATCTTCTGAAG	2501
QY	2478	AGTACATGCCCTTCATGAAATTCAGTTTGTCTATGCAATCAGGAAGGTTTTAAAGAAC	2537
Db	2502	AAGTCGAACCTTTTGTCAAAGTACAGTATATCTATNGGCATCAGCAAGCTTCTACGAGC	2561
QY	2538	AGGGAAACAGAGCTCGTGAATTTTGGAAAGTAGCGGCTCTTGTGAATCTTGTGCTTACCTATCG	2597
Db	2562	GTCAATGCTGAAGGACGCGCTTCAATAAAGCGAGCTTATCAACGTAGAGATTCCTATAG	2621
QY	2598	GGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTACAATCTAATCTCTTGGTT	2657
Db	2622	CGCTCAGCTTCGAAAGAGACTCAAAATCAGAAAAGGGAATTAACGATCTTACTCTTATGT	2681

RESULT 14

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US-10-282-122A-18495
; Sequence 18495, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18495
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-18495

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QY 101 ATGAAGTCTTCTTTCCCAAGTTGTATTTTCTACATTTGCTATTTTCCCTT---TGTCCT

1 ATGAAGTCCTCTGTCTCTTGTTGTTCTTTCTTCAATCCCGCTCTTTTCATCGCTCTCT 60
158 ATGATTGCTACCGAGACAGTTTGGATTTCAAG---TGGAGATTTCGATGGGAATAAAAT 214
61 ATAGTCGCGCAGAGGTGACCTTAGATAGCAGCAATAATAGCTATGATGATCTAAACGGA 120
215 GGTAAATTTTTCAGTTCGTGAGAGTCAGGAAGTCT--GGAACCTACCTACCTATTAAAG 271
121 ACTACTTTCAGGTCTTTTCCACTACGACGCTGCTGAGGAACCTACTATTCTCTTACTT 180
272 GGAATATGTCACCTAGAAATATTTCTCGAACAGGCACAGCAATCAAAAGAGCTGTTTT 331
181 TCCGACGTATCTTTTCAAAATGACGGGCTTTAGGAATTCCTTAGCCTCAGGATGCTTC 240
332 AACAACTAAGGGGATTTGACTTTTCAAGGTAAACGGGAACCTCTATTGTTTCCAAAG 391
241 CTAGAAGCGGGCGGATCTTACTTTTCCAAAGGAATCAACATGCATCTGAAGTTTGCAAT 300
392 GTGGATGCAGGACTGTAGCAGGGCTGCTGTTAAACAGACGCTGGTAGATAAATCTACC 451
301 ATCAATGCGGGCTCTAGCGCTGGAACCTGTAGCCAGTACCTCAGCAGCAGATAGAATCTT 360
452 ACGTTTATAGGGTTTCTTCGCTATCTTTTATTTGCGTCTCTCGAAAGTTCGATACTACC 511
361 CTCCTTAAATGATTTTCTAGACTCTCTATTATCTCTGTCCCTCTCTTCTCTCTCTCT 420
512 GGCAAAGGACCGTTAGTCTCTACGGGTAGCTTGGATTTGACAAAATGTCAGTTTG 571
421 ACTGGAATATGCTTTAAATCTGTGGGAATCTATCTCTAACTGGCAATCTCCAAAT 480
572 CTCCTCAGCAAAATCTTTCAACGGATAATGGGGTGTATCAACCGCAAAATCTTTTCA 631
481 ATATTTACTCAGAACTTCTCGTCAGATACGGGGTGTATCAATACGAAAACTTCTTA 540
632 TTAAACGGGACTCAATGTCAAGTCTGTGTTTCTGAAAATACCTCTCT-----CAAGAAA 685
541 TTATCAGGACATCTCAGTTTGGAGCTTTTCAGAAACCAAGCTTTCACAGGGAAGCAA 600
686 GCGGAGCCATTCAGACTTCGATGCGCTTACCAATTAAGTCAAGGAGGAGTCTCT 745
601 GCGGGTGATTTACGCTACAGGAATATAACTATCGAGAACACGCCCTGGGATAGTTTC 660
746 TTTTCTGACAAATCTCTTCGGATTCGGAGCTGCAATTTTACAGAAAGCCTCGTGACT 805
661 TTTCTCAAAACCTAGCGAAAGGATCTGGGGTGTCTGTACGACCTGACAACTGTTCG 720
806 ATTTCTAATAATGCTAAAGTTTCCTTTATGCAATAAGTCTACAGAGCGAGCTCTCA 865
721 ATTACAGATAAATTTCAAGTGATCTTTGACGGCAATAGTGTGCGGAAGCGCTCAAGCT 780
866 ACAACGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAG 925
781 CAGGGCGGGCTAT-----TTGTTGCACTACGACAGATAAAACA 819
926 GTCAACCTCTACTGGAATCAGATGTTACTCTTCAGCAACATAATCATCGAACAGCGGGA 985
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986 GGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCGGAGGACTTACCCTATTTCAGTAGA 1045
880 GGAGCCATCTCTGACTCAAGGTCAAGTATTTCCGCTGGAGGTCTCTCTATTTCAAAGT 939
1046 AATAGTGTCAATGAGGTACAGTCTCT---CTAAAGGTGGAGCCATAGCTATCGAAGATAGT 1102
940 AATATCTCAGGAAGTAGCGCGGT CAGGGAGGAGGAGCGATCAATATAGCATCTGCT 999
1103 GGGGAATGAGTTTATCCCGCGTAGTGGTCAGATGTTCTTTTTTAGGGAATACAGTCACT 1162
1000 GGGGAAGTCTGCTCTCTCTGCTACTCTCTGAGATATTTACCTTCAATACAAACAGTCAAC 1059
1163 TCTACTACTCTCGGAGCAATAGAAAGTAGTATCGACTTTAGGAACGAGGTGCAAGATGACA 1222
1060 AACGGAAGCAAGTACAGAAACCGCAATAAATATATTGATACC---GCTAAAGTCACA 1116

1223 GCTTTGCGTTCTGCTGCTGTAGGCCATCTACTTCTATGATCCCATAACTACAGGATCA 1282
1117 TCGATACGAGCTGTCTACGGGCAATCTATCTATTCTATGATCCCATCAAAATCAGGA 1176
1283 TCCACAACAGTTTACAGATGCTTTAAAGTTAATGAGACTCCGGCAGATTCTGCACTACAA 1342
1177 ACGGAGCTTCTACCGACACATTTGAACCTTAGCAGATCGGAACAGTGAATCGAG 1236
1343 TATACAGGGAACATCATCTTTCACAGGAGAAAGTTATCAGAGACAGAGCGCGCAGATTCT 1402
1237 TATGGGGGTGCGATTTGCTTTTCTGGAGAAAGCTTTCCCTTACAGAAAAGCAATGCGT 1296
1403 AAAAACTTACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGAGTACTTATCTTTA 1462
1297 GCAACGTCACCTCTACTATCCGAACTCTGAGTATTAGCGCGGGAGATCTTGACTT 1356
1463 AAACATGGAGTGACTCTGAGACTCAGGCATTCACCTCAACAGGCAGATTCTGCTCGAA 1522
1357 CGTGATGGAGTCAACCGTAACCTTTCAAGGATCTGACTCAAAGTCCAGGATCCCGCATCTTA 1416
1523 ATGCACTAGGAACCTACTCTAGAACCT---GCTGATACTAGCACCATAACAATTTGGTC 1579
1417 ATGGATGGGGGACTACACTTAGTCTAAAGAGGCAAACTTTTCGCTTAATGCTTAGCA 1476
1580 ATTAACATCAGTTTCTATAGACGGTGCAAAAGAGGCAAAATAGAAAACCAAGCTACGTCA 1639
1477 GTAATCTCTCTCTTTAGATGGAACCAACAGGAGCTTTAAACACAGAGCTGCAGAT 1536
1640 AAAAACTGACTTTATCTGGAACCATCACTTTATGGACCCGACGGGCAGCTTTTATGAA 1699
1537 AAAAAATACAGCCTATCGGGAACGATTGCGCTTATTGACACGGAAGGTCATTCTATGAG 1596
1700 AATCATAGTTTAAAGAACTCTCAGTCTCTAGCATCTTAGAGCTCA-----AGCT 1750
1597 AATCATAACTTAAAAAGTGTAGTACTCTCTCTTTGAACTTACCACCGCAGGAGCC 1656
1751 TCTGGAACTGTAAACAGCACCGCAGTGACTCCAGATCTCTATAATGGTGAGAAATTCAT 1810
1657 AACGGAAGATTAATCTGAGGAGCTCTTTCTACCTGACTCTTCAAGAACCTGAACCCAC 1716
1811 TAGCGCTATCAGGGAACCTGGGGCCCAATTTGTTGGGGGACAGGGGCTTCTACGACTGCA 1870
1717 TAGCGGTATCAAGSAAACCTGCGAGTTGTCTTGGGCAAAATGCAACATCTCAAAAATAGGA 1776
1871 ACCTTCAACTGGACTAAACCTGCTATATCTCTAAATCCCGAGCGTATCGGCTCTTTAGTC 1930
1777 AGCATCAACTGGACCCGTCACAGGATACATTCCTTAGTCTCTGAGAGAAAAGTAATCTCCCT 1836
1931 CCTAATAGCTTATGGAATGCATTTATAGATATTTAGTCTCTCTCCATTTATTTATGGAGACT 1990
1837 CTAATAGCTTATGGGAAACCTTTATAGATATACGCTCGATCAATCAGCTTATAGAAACC 1896
1991 GCAACGAAGGGTTGACGGAGACCGGTCTTTTGGTGTGCTGGATTTATCTAATCTTCTTC 2050
1897 AAGTCCAGTGGGAGCCCTTTTGAGCGTGAAGTATGGCTTTTCAAGAAATGGGAATTTCTTC 1956
2051 CATAGGATAGTACAAAACACGACCGGGTTTTCGCCATTTGAGTGGCGGTATGTCATA 2110
1957 TATAGGATTTCTATGCCACCCGCAATGGTTTCCGCCATATACGCGGGGTATGCACTA 2016
2111 GGAGGAACCTACATCTCTTTCAGATAAGATTTCTTAGTGTGCTGATTTTGTCACTCTTTT 2170
2017 GGGATCACGCAACATCTCTCGGAGGATCAGTCTACTTTTGGCTTCTGCCAGCTCTTT 2076
2171 GGAAGGATAGAGACTATTTTGTAGCTAAGAACTAAGGTACAGTCTACGAGGAACCTCTC 2230
2077 GCTAGAGATCGCAATCATATTTACAGGTAAAGAACCAAGGAGATATCTACGGTGCCTCTTG 2136
2231 TATTACAGCA-----CAACGAACCTATATCTCTCTCTCTCTCTGCAAA 2272
2137 TATTTCCACATACAGAAAGGCTCTTCGACATCGCAATTTCTCTCTGGGAAAAGCAACC 2196

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QY 2273 CTACGGCCCTGTTGGTCTTATGTTCTCTACAGAGATTCCTGTTCTCTTTTCAGAAAC 2332
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QY 2197 CGAGTCCCTGGGTGCTCTCTGAGATCTCCAGATCAATTCCTTATCGTTCGATGCTAAA 2256
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QY 2333 CTTAGCTACACCATACGATTAACGATCTGAAACCAAGTATACACATATCCTACTGTT 2392
Db      |||
QY 2257 TTCAGTTATCTCATACAGCAACACACATGAGACATATATACCGATCACTCTATCATC 2316
Db      |||
QY 2393 AAAGGAAGCTGGGGGAAGATAGTTTCGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGC 2452
Db      |||
QY 2317 AAGGGTCTCTGGAGAAACATGCTTCTCTGCGAGATCTTGGAGCTAGCCCTGCTTTGTT 2376
Db      |||
QY 2453 TTAGATGAAGTCTCTATTTGAGCGATACATGCCCTCATGAATTCGAGTTGCTAT 2512
Db      |||
QY 2377 ATTTCCGTTCCGTATCTCTGAAAGAGTCGAACCTTTTGTCAAAGTACAGTATATCTAT 2436
Db      |||
QY 2513 GCACATCAGAAAGGTTTTAAAGAACAGGGAACAGAAAGCTCGTGAATTTTGGAAAGTAGCCGT 2572
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QY 2437 GCGCATCAGCAAGACTTCTACAGCGTCACTGTAAGGACGCGCTTCAATTAAGCGAG 2496
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QY 2753 CAAAGCTTTAGTCTTCGTCGAGGAAACCAATTTTGGTTTCTTAACTCAAAATTTGAAGCCTTT 2812
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QY 2677 CAAAGTTTTCTGTTGCTCGAACCATTTCGAAGTGAACCCCAATGGAATCTTTC 2736
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QY 2813 AGCCAAATTTCTTTGAATGCGTGGTCACTCTCGCAATTAAGTACGACTTAGGAGA 2872
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QY 2737 GGTCAATTCGCTTTTGAAGTACGAAAGTTCTTCAAGAAATTAATACAAACCTAGGCTCT 2796
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RESULT 15

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US-10-312-273-154
; Sequence 154, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
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; SEQ ID NO 154
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-154
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Query Match 16.8%; Score 503.6; DB 16; Length 2811;

Best Local Similarity 51.4%; Pred. No. 1.1e-131;

Matches 1458; Conservative 0; Mismatches 1304; Indels 72; Gaps 10;

QY 101 ATGAGTCTTCTTCCCAAGTTTCTATTTCTACATTTGCTATTTTCCCTT---TGCTT 157

Db 1 ATGAAAGTCTCTGTCTCTTGGTGTCTTTCTTCAATCCCGCTCTTTTCATCGCTCTCT 60

QY 158 ATGATTGTCTACGAGACAGTTTGTGATTCAG---TGCAGTTTCGATGGGAATAAAAAAT 214

Db 61 ATAGTCGGCGCAGAGGTGACCTTAGATAGCAGCAATAATAGTATGATGATGATTAACGA 120

QY 215 GGTAAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAATCTACCTACCTATTAAAG 271

Db 121 ACTACCTTTCACGGTCTTTTCCACTACGACGCTGCTGCAGGAACCTACCTATTCTTACTT 180

QY 272 GGAATGTCACTCTAGAAAAATATTCCTGGAACAGCACAGCAATCACAAAAAGCTGTTTT 331

Db 181 TCCGAGTATCTTTTCAAAATGACAGGCGCTTTAGGAATTCCTTAGCTCAGATGCTTC 240

QY 332 AACACACTAAGGGCGATTTGACTTTTACAGGTAAACGGGAACCTCTATTGTTCCAAACG 391

Db 241 CTAGAAGCGGCGCGATCTTACTTTTCCAAGGAATCAACATGCATGCAAGTTTGCATTT 300

QY 392 GTGGATGAGGAGACTGTAGCAGGCGCTGTTTAAACAGCAGCGTGGTAGATAAATCTACC 451

Db 301 ATCAATCGGGCTCTAGCGCTGGAACTGTAGCAGTACCTCAGCAGCAGATAAGAACTCT 360

QY 452 AGTTTTATAGGTTTTCTTTCGCTATCTTTTATTTGCTCTCTCTGGAAGTTTCGATACTACC 511

Db 361 CTCCTTAATGATTTTCTAGACTCTCTATATCTCTTGTCCCTCTCTCTCTCTCTCTCT 420

QY 512 GCAAGAGGCGGTAGTCTCTACGGGTAGCTTGTGAGTTTGACAAAAATGTCAGTTTG 571

Db 421 ACTGGACAATGTCTTAAATCTGTGGGAATCTATCTTAATCTGGCAATTTCCCAATTT 480

QY 572 CTCCTCAGAAAACTTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCTTTCA 631

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QY 632 TTAACAGGAGCTACAAATGTCAGCTCTGTTTTCTGAAAAATACCTCTCT---CAAGAAA 685

Db 541 TTATCAGGAGCATCTCAGTTTGGAGCTTTTTCGAGAAACCAAGCTTTCACAGGGAAGCA 600

QY 686 GCGGAGCCATTTCAGACTTCCGATGCCCTTACCATTACTTGGAAACCAAGGGGAAGTCTCT 745

Db 601 GCGGTGTAGTTTACGCTACAGGAATATACTATCGAGAAACAGCCCTGGGATAGTTTCC 660

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Db 661 TTCTCTCAAAACCTTAGCGAAAGGATCTGGCGGTGCTCTGTACAGCACTGACAACTGTTG 720

QY 806 ATTTCTAATAATGCTAAAGTTTCTTTTATTCACATAAAGTTCACAGGAGCGAGCTCTCA 865

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QY 866 ACAAGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGATACTAAG 925

Db 781 CAGGGCGGGCTAT-----TTGTTGCACTTACGACAGATAAAAAA 819

QY 926 GTCACCTCTCCTGGAATCAGATGTTTCTTTCAGCAACATACATCCACACACAGCGGA 985

Db 820 GTGACTCTTACTGGGAACAAAAACCTCTCTTTTCAAAATAATACAGCATATGATGCG 879

QY 986 GGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCGGGAGGACTTACCTCTTTCAGTAGA 1045

Db 880 GGAGCCATCTCTGGACTCAGGTCAAGTATTTCCCGTGGAGGTCTCTACTTATTTCAAAGT 939

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QY 940 AATATCTCAGGAAGTAGCGCGGTCAAGGAGGAGGAGCGATCAATATAGCATCTGCT 999
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QY 1103 GGGGAATTGAGTTATCCGCCGATAGTGTGAGCAATGTCTTTTAGGGAATACAGTCACT 1162
Db |||||
QY 1000 GGGGAATCGCTCTCTCTGCTACTTCTGGAGATATACCTTCAATAACACCAAGTCAAC 1059
Db |||||
QY 1163 TCTACTCTCTGGAGCAATAGAAAGTATCGACTTAGAAACGAGTGCAGAGATGACA 1222
Db |||||
QY 1060 AACGGAAGCAACAAGTACAAGAAACGCAATAAATATCATTTGATACC---GCTAAGTCA 1116
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QY 1223 GCTTTGCGTTCTGCTGTGTAGAGCATCTACTTCTATGATCCCAATACAGGATCA 1282
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QY 1117 TCGATACGAGTGTCTAGGGGCAATCTATCTATTTCTATGATCCCAATCAAAATCCAGGA 1176
Db |||||
QY 1283 TCCACAACAGTTACAGATGTCTTAAAGTTAAATGAGACTCCGGCAGATTTCTGCACATCAA 1342
Db |||||
QY 1177 ACCGAGCTTCTACCGACACATTTGAACCTTAACTTAGCAGATGCGACAGTGCAG 1236
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QY 1343 TATACAGGAACATCATCTTCAAGAGAAAGTATACAGAGACAGAGCGCGAGATPTCT 1402
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QY 1237 TATGGGGTGCATGTCTTCTCGAGAAAGCTTTCCCTACAGAAAAAGCAATCGCT 1296
Db |||||
QY 1403 ABAATCTTACTTCGAGCTACTACAGCCTGTAACTCTTTCAGAGGTACTCTATCTTTA 1462
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QY 1297 GCAACGTCACCTCTACTATCCGACAACTGCGAGTATAGCGGGGAGATCTTGTACTT 1356
Db |||||
QY 1463 AAACATGGAGTACTCTGCACTCAGGCATTTCACTCAACAGGAGAGATTTCTGCTCTGAA 1522
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QY 1357 CGTGATGGAGTCAACGTAACCTTTCAAGGATCTGACTCAAGTCCAGGATCCCGCATCTTA 1416
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QY 1523 ATGCACTGAGAACTACTCTAGAACCT---GCTGATCTAGCACCATAAACAATTTGGTC 1579
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QY 1417 ATGGATGGGGGACTACACTTAGTGTCTTAAAGAGCAAACTCTTTCGCTTAATGGCTTAGCA 1476
Db |||||
QY 1580 ATTAACATCAGTTCTATAGACGGTGAAGAGGCAAAATAGAAACCAAGCTACGTCA 1639
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QY 1477 GTAATCTCTCCTCTTTAGATGGAACCAACAGAGCAGCTTTAAACACAGAGCTGCAGAT 1536
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QY 1640 AAAAACTGACTTTATCTGAAACCATCACTTTTATTTGACCCGACGGGCAAGTTTATGAA 1699
Db |||||
QY 1537 ABAATATCAGCTATCGGNAAGATTTGCGCTTATTTGACACGGAAGGTCTATCTATGAG 1596
Db |||||
QY 1700 AATCATAGTTTAGAAATCTCAGTCTCTAGACATCTTAGAGTCA-----AAGCT 1750
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QY 1597 AATCATAACTTAAAGTGTGTAGTACCTATCTCTTCTTGAACCTTACCAACCGCAGGAGCC 1656
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QY 1751 TCTGGAACTGTAAACACCGCAGTCACTCCAGATCCTATATGCGGTGAGAAATTCAT 1810
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QY 1657 AACGGAACGATTTCTCTGGAGCTCTTTCTACCTCTGACTTTCAAGAACCTGAAACCCAC 1716
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QY 1811 TAGCGTATCAGGAACTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTCTACGACTGCA 1870
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QY 1717 TAGGGTATCAAGGAATCTGCACTTGTCTTGGCAATGCAATCTCTCAAAATAGGA 1776
Db |||||
QY 1871 ACCTTCACTGGAATAAACTGGCTATATCTCTAATCCGAGCGTATCGGCTCTTTAGTC 1930
Db |||||
QY 1777 AGCATCAACTGGACCGCTACAGGATACATCTCTAGTCTGAGAGAAAGATTAATCTCCCT 1836
Db |||||
QY 1931 CCTAATAGCTTATGGAATGCAATTTATAGATATAGTCTCTCCATTTCTTATGAGACT 1990
Db |||||
QY 1837 CTAAATAGCTTATGGGAAACCTTTATAGATATAGCTCGATCAATCAGCTTATAGAAACC 1896
Db |||||
QY 1991 GCAACGAAGGTTTCAGGGAGACCGTCTTTTGGTGTGCTGATTAATCTAACTTCTTC 2050
Db |||||
QY 1897 AAGTCCAGTGGGAGCCTTTTGGCGGTGAGCTATGGCTTTTCAGGAATTCGAAATTTCTTC 1956
Db |||||
QY 2051 CATAGAGTAGTACAATAACACGAGCGGGTTTCGCCATTTGAGTGGCGGTTATGTCA 2110
Db |||||
QY 1957 TATAGAGATTCTATGCCCAACCCGCGCATGGTTTCGCCCATATCAGCGGGGGTTATGCATA 2016
Db |||||
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QY 2111 GGAGGAAACCTACATACTTTGTTTCAGATAAGATTTCTTAGTCTGCTGATTTTGTGAGCTCTTT 2170
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QY 2017 GGGATCAGCAACAACCTCTCTCGAGGATCAGCTTACTTTTGGCTTCTGCCAGCTCTTT 2076
Db |||||
QY 2171 GGAAGAGATAGAGACTACTTTTGTAGTAAAGATCAAGGTACAGTCTTACGAGGAGAACTCTC 2230
Db |||||
QY 2077 GCTAGAGATCGCAATCATATTACAGGTAAAGAACCGAGATACTTACGGTGCCTCTTTG 2136
Db |||||
QY 2231 TATTACAGCA-----CAACGAAACCTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2272
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QY 2137 TATTTCCACCATACAGAAAGGCTCTTCGACATCGCAATTTCTCTGGGAAAGCAACC 2196
Db |||||
QY 2273 CTACGGCTTTGTTGTTCTTATGTTCTTACAGAGATTCCTGTCTCTCTCTCTCTCTCTCTCTCT 2332
Db |||||
QY 2197 CGAGTCCCTGGGTGCTCTCTGAGATCTCCAGATCATTTCTTTATCGTTCGATGCTAAA 2256
Db |||||
QY 2333 CTTTGTACTACACCATACGGATAACGATCTGAAACCAAGTATACAAATATCTTACTGTT 2392
Db |||||
QY 2257 TTCAGTTATCTCCATACAGACAACCATGAAGACATATTATACCGATAACTCTATCATC 2316
Db |||||
QY 2393 AAAGGAAGCTGGGGGATGATGTTTCGTTTGAATTCGTTGGAAGAGCTCCGATTTGC 2452
Db |||||
QY 2317 AAGGGTTCTTTGGAGAACGATGCTCTGTGCGAGATCTTGGAGCTAGCCCTGCTTTGTT 2376
Db |||||
QY 2453 TTAGATGAAAGTGTCTTATTTGAGCAGTACATGCCCCCTTCATGAAATTCAGTTTGTCTAT 2512
Db |||||
QY 2377 ATTTCCGTTCCGTATCTTCTGAAAGAGTCAACCTTTTGTCAAAGTACAGTATATCTAT 2436
Db |||||
QY 2513 GCACATCAGGAAGGTTTTAAAGAACAGGGAAACAGAGCTCGTGAAATTTGGAAGTGCCT 2572
Db |||||
QY 2437 GCGCATCAGCAAGACTTCTACAGAGCGTCACTGTGAAGGACGCGCTTTCAATAAAAGCGAG 2496
Db |||||
QY 2573 CTTTGTGAATCTTGGCTTACCTATCGGATCCGATTTGATGAAGTACAGTCCGAGAT 2632
Db |||||
QY 2497 CTTATCAACGTAGAGATTCCTATAGGCGTCACTTGGAAAGAGACTCAAAATCAGAAAG 2556
Db |||||
QY 2633 GCAACGTACAAATCTAATCTTGTGTTATCTGTGATCTTGTCTGTAGTAAACCCGACTGT 2692
Db |||||
QY 2557 GGAATCTTACGATCTTACTCTTATGTTATATCTCGATCTTACCGACGCAATCTTAATGT 2616
Db |||||
QY 2693 ACAGACAACACTCGGAATTAGCGGTGATTTTGGAAAACTTTCGGTACGAAATTTGGCAAGA 2752
Db |||||
QY 2617 CAAACTTCCCTAATAGCTAGCGATGCTAACTGGATGGCTTATGGTACCAACCTCGCACGA 2676
Db |||||
QY 2753 CAAGCTTTAGTCTCTCGTCAGGAGGACCAATTTTGTCTTAACTCAAAATTTTGAAGCCTTT 2812
Db |||||
QY 2677 CAAGGTTTTTCTGTGCTGCGAACCAATTCAGTGAACCCCACTGGAATCTTC 2736
Db |||||
QY 2813 AGCCAAATTTCTTTTGAATTCGCTGGGTCTATCTCGCAATTCAAATGTAGACTTTAGGAGCA 2872
Db |||||
QY 2737 GGTCAATTCGCTTTTGAAGTACGAGTTCTTACGAAATTTAATACAAACCTTAGGCTCT 2796
Db |||||
QY 2873 AAATACCAATCTA 2886
Db |||||
QY 2797 AAGTTTTGTTCTA 2810
Db |||||
```

Search completed: August 16, 2004, 21:06:33
Job time : 924 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:07:10 ; Search time 14 seconds
(without alignments)

3451.507 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSSFPKVFSTFAIFPLSM.....FELRGSSRNYNVDLGAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2058	43.1	328	1 PM10_CHLPN	Q9r565 chlamydia p
2	1982	41.5	328	1 PM9_CHLPN	Q9z398 chlamydia p
3	1964	41.1	336	1 PM7_CHLPN	Q9z898 chlamydia p
4	1936	40.6	930	1 PM8_CHLPN	Q9z393 chlamydia p
5	1855	38.9	928	1 PM11_CHLPN	Q86164 chlamydia p
6	1573	32.9	841	1 PM2_CHLPN	Q9z3a1 chlamydia p
7	1444	30.2	1276	1 PM6_CHLPN	Q9z899 chlamydia p
8	1442.5	30.2	922	1 PM1_CHLPN	Q9z295 chlamydia p
9	1377.5	28.9	973	1 PM13_CHLPN	Q9z896 chlamydia p
10	1120.5	23.5	1013	1 PMPG_CHLTR	Q84879 chlamydia t
11	1051	22.0	987	1 PMPG_CHLTR	Q9p145 chlamydia m
12	911	19.1	867	1 PMF1_CHLMU	Q9p141 chlamydia m
13	863	18.1	878	1 PMF1_CHLTR	Q84882 chlamydia t
14	685.5	14.4	1609	1 PM21_CHLPN	Q9z265 chlamydia p
15	667.5	14.0	978	1 PM14_CHLPN	Q9z895 chlamydia p
16	666	14.0	947	1 PM19_CHLPN	Q9z813 chlamydia p
17	666	14.0	1723	1 PM20_CHLPN	Q9z812 chlamydia p
18	665.5	13.9	946	1 PM18_CHLPN	Q9z880 chlamydia p
19	647	13.6	952	1 PM16_CHLPN	Q9z882 chlamydia p
20	603.5	12.6	938	1 PM5_CHLPN	Q9z883 chlamydia p
21	603	12.6	975	1 PMPA_CHLTR	Q84417 chlamydia t
22	597	12.5	1016	1 PMPH_CHLTR	Q84880 chlamydia t
23	594	12.4	980	1 PMPH_CHLMU	Q9p144 chlamydia m
24	587.5	12.3	976	1 PMPA_CHLMU	Q9p143 chlamydia m
25	576.5	12.1	1531	1 PMPD_CHLTR	Q84818 chlamydia t
26	559	11.7	1754	1 PMPB_CHLTR	Q84418 chlamydia t
27	549	11.5	976	1 PMPE_CHLMU	Q9p147 chlamydia m
28	548.5	11.5	1672	1 PMPB_CHLMU	Q9p147 chlamydia m
29	544	11.4	1520	1 PMPD_CHLMU	Q9p1b0 chlamydia m
30	541.5	11.3	964	1 PMPE_CHLTR	Q84877 chlamydia t
31	533.5	11.2	1460	1 PMPC_CHLMU	Q9p1j1 chlamydia m
32	523	11.0	1770	1 PMPC_CHLTR	Q84419 chlamydia t
33	490	10.3	1034	1 PMPF_CHLTR	P38008 chlamydia t

RESULT 1

ID	PM10_CHLPN	STANDARD;	PRT;	928 AA.
AC	Q9r565; Q86163; Q9RB64; Q9S6P2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Probable outer membrane protein pmp10 precursor (Polymorphic membrane protein 10) (Outer membrane protein 5).			
GN	PM10 OR OMP5 OR CP0303 OR CPB0467.			
OS	Chlamydia pneumoniae (Chlamydophila pneumoniae).			
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.			
OX	NCBI_TaxID=83558;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=VR1310;			
RX	MEDLINE=20007584; PubMed=10539856;			
RA	Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,			
RA	Madsen A.S., Knudsen K., Falk E., Birkelund S.;			
RT	"Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity.";			
RL	Am. Heart J. 138:S491-S495(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AR39;			
RX	MEDLINE=20150255; PubMed=10684935;			
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,			
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,			
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,			
RA	Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,			
RA	Eisen J., Fraser C.M.;			
RT	"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";			
RL	Nucleic Acids Res. 28:1397-1406(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=J138;			
RX	MEDLINE=20330349; PubMed=10871362;			
RA	Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,			
RA	Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;			
RT	"Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWU029 from USA.";			
RL	Nucleic Acids Res. 28:2311-2314(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TW-183;			
RA	Geng M.M., Schumacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,			
RA	Schneider S., Pohl T., Essig A., Marre R., Melchers K.;			
RT	"The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 1-914 FROM N.A.			
RC	STRAIN=CWL029/VR-1310;			
RX	MEDLINE=99081766; PubMed=9864239;			
RA	Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;			

Q9z3d6 chlamydia p
Q9p146 chlamydia m
P15921 rickettsia
Q52657 rickettsia
P35828 caulobacter
P47033 saccharomyc
P18305 chilo iride
P35827 campylobact
P96989 r outer mem
Q53020 r outer mem
P40442 saccharomyc
P45508 escherichia

Nucleic Acids Res. 28:1397-1406(2000).

[4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shizai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=TW-183;
 RA Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Basig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 RT other Chlamydia strains based on whole genome sequence analysis";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC -----
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 CC -----
 DR EMBL; AJ133034; CAB37069.1; -
 DR EMBL; AB001628; AAD18591.1; -
 DR EMBL; AB002192; AAF38163.1; -
 DR EMBL; AB002546; BAA98655.1; -
 DR EMBL; AB017158; AAF98395.1; -
 DR PIR; B72077; B72077.
 DR PIR; E86546; E86546.
 DR TIGR; CP0306; -
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; Chlamydia PMP; 2.
 DR TIGRFAMS; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMS; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 928 PROBABLE OUTER MEMBRANE PROTEIN PMP9.
 SQ SEQUENCE 928 AA; 98332 MW; 58910A8F04F12219 CRC64;

Query Match 41.5%; Score 1982; DB 1; Length 928;
 Best Local Similarity 45.2%; Pred. No. 4.4e-100;
 Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;

QY 1 MKSSPFKVFSTFAIPLSM-----IATETVLDSASFQDNKGNFVSRESQEDA-GTT 53
 DB 1 MKSSLHFWLISLSLALPLSFAAPAAVVEINLGPINSFSG--PGITYTPAQTADGII 58
 QY 54 YLFKGNVTLENIPTGTATKSCFNNTKGDLTFTTGNLNLFFQTVAGVAGAVNSVV 113
 DB 59 YNLTDGVSITN-AGSPALTATSCFKETGNLSFQGHGYQFLQNDAG--ANCTFTNTAA 115
 QY 114 DKSTTFIGSSLSFIASPGSIITTGAVSCSGSLTKNVLSLFFSKNFTSDNGGAI 173
 DB 116 NKLLSFGSGLYLIQT--TNATITGAIK-STGACISQSNYSYCFQGNFSDNGGALQG 172
 QY 174 KTLSTGTTMSALFSENTSSKKGAIQTSDALITGNQGVFSFSDNTSSDGAIFTEAS 233
 DB 173 SSISLS-LNPNLTFAKNKATQKGALYSTGCIITNNTLSASFSENTAANNNGAIY 231
 QY 234 VTISNNAKVSFINKVTYGASSSTTGMDSGGAICAYKTSTDTKV-TLTGNQMLFSSNTST 292
 DB 232 SFISNNKAISFINNSVTATSA-----TGGAICYCSSTSAKPVPVLTLSNDGELNFIGNTAI 285

QY 293 TAGGAIYVKKLELASGGLTLFSRNSVNGCTAPKGGAIATIEDSGELSLSADSGDIVELGNT 352
 DB 286 TSGGAIYTNLVSSGGPTLFKNNSAIDTAAPLGGAIATADSGLSLSALGGDITEGNT 345
 QY 353 V---TSTTEGTRNRSSIDLG-TSAKMTALSAAGRAIFYDYDPITTGSSSTTVTVLKVNETP 408
 DB 346 VVKGASSQTTRNSINIGNTNWKIVQLRASQGTIYFYDPIITTSITAAALSDALNLGPD 405
 QY 409 ADSALQYTGNIIFTGKLESETAADSCKNTSKLQVPTLSSGGTSLSKHGVTLOQTQFTQ 458
 DB 406 LAGNPAYQGTIYFSGEKLSEAAEADNLKSTIQOELTLAGQLSKSGVTLVAKFSQS 465
 QY 469 ADSRLEMDVGTTELEPADTSTINNLVINISSIDAKKAKIETKATSKNLTLSGTTILDDPT 528
 DB 466 POSTLLMDAGTILETAGDITINNLVNVDSLKETKATIKATQASQTVILSGSLSLVDP 525
 QY 529 GTFYENHSLRNPQSDILELKAS--GTVTSTAVTPDPIMGEKPHYGYQGTWGIWGTGA 586
 DB 526 GNVYEDVSNWNPQVFSCLTLTADDPANIHTDLAADPLEKNPIHMGYQGNWA-LSWQEDT 584
 QY 587 ST---TATFNWTKTYIPNPERIGSLVPSNLNNAFIDISLHVMETANEGLOGDRAFWC 643
 DB 585 ATKSKAATLTWTGTGNPNPERGTLVANTLWGSFVDVRSIQOLVATKVRQSETGICW 644
 QY 644 AGLSNPFHKDSTKTRGFRHLGGVYIGNLTCSDKILSAAFCQLFGRDRDYFVAKNOG 703
 DB 645 EGISNPFHKDSIKNGFRHISAGYVVGATTILASDNLITAAFCQLFGKDRDHFINKRA 704
 QY 704 TVYGGTLYYOHNETYISLPCRLRPSLSYVP---TEIPVLFSNLSYTHTDNLKTKYTT 760
 DB 705 SAYAASLHLQHLATLSS-----PSLLRYLPGSESPQVLFDAQISYISKNTMKTYITQ 758
 QY 761 YPTVKSGWGNDSFALFEGGRAP-ICLDESALFQYMPFMKLPFYVAHOBGFKEQGTE-AR 818
 DB 759 APKGSSWYNDGCALEASSLPHLTHSGLHAYFPFIKVEASYIHQDSFKERNITLVR 818
 QY 819 EFGSSRLVNLALPIGIRFDKESDCQDATYNLTGYTVDLVRSNPDCCTTLRLISGDSWKTF 878
 DB 819 SFDSDGLINVSVPIGITFERFSRNERASYEATVIYVADVVRKNPDCCTTALLNNTSWKTT 878
 QY 879 GTNLARQALVLRAGNHFCSNFSAFQSFELRGSSRNYNVDLGAKYQF 928
 DB 879 GTNLSRQAGIGRAGIFYAFSPNLVTSNLSMBIRGSSRSYNADLGKGFQF 928

RESULT 3
 PMP7 CHLPN STANDARD; PRT; 936 AA.
 ID AC Q92898; Q9J542; Q9Z504;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable outer membrane protein pmp7 precursor (Polymorphic membrane
 DE protein 7) (Outer membrane protein 12).
 GN Pmp7 OR OMP12 OR CPN0445 OR CP0308 OR CPB0462.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.
 NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR33;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.,
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.",
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.",
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW-183;
 RA Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 RT other Chlamydia strains based on whole genome sequence analysis.",
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 658-936 FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RT role in immunopathogenicity";
 RL Am. Heart J. 138:S491-S495(1999).
 CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (potential).
 CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
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 DR EMBL; AE001627; AAD18589.1; -;
 DR EMBL; AE002193; AAF38165.1; -;
 DR EMBL; AF002546; BAA98653.1; -;
 DR EMBL; AE017158; AAP98393.1; -;
 DR EMBL; AJ133034; CAB37067.1; -;
 DR PIR; B81591; B81591.
 DR PIR; C72078; C72078.
 DR PIR; C86546; C86546.
 DR PHCI-2DPAGE; Q9Z898; -;
 DR TIGR; CP0308; -;
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR003368; Chlamydia PMP.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF02415; Chlamydia PMP; 2.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP-repeat; 6.
 DR Outer membrane; Signal; Multigene family; Complete proteome.
 KW SIGNAL
 FT CHAIN 1 23
 FT PROBABLY OUTER MEMBRANE PROTEIN PMP7.
 FT PTHGFRHI -> EDNIYRHN (IN REF. 5).
 FT Y -> H (IN REF. 1, 4 AND 5).
 FT CONFLICT 658 666
 FT CONFLICT 822 822
 SQ SEQUENCE 936 AA; 100105 MW; 3981DB3C950AF95A CRC64;
 Query Match 41.1%; Score 1964; DB 1; Length 936;
 Best Local Similarity 43.4%; Pred. No. 4.2e-99;
 Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;
 QY 1 MKSSPPKFFVSTFAIF-PLSMATATVLDSS-ASFDGKNGNFSVRESQE-DAGTYLLEK 57

Db 1 MKSSVSWLFFSSSIFLFSLSIAVAEVLTDSSNNYSYDGSNGTFTVFSTDDAAAGTYSL 60
 QY 58 GNVLTENIPGCTGTAITKSCFNNTKDGTLFTTNGNSLLPOTVDAGTVAGAAVNSSVVDKST 117
 Db 61 SDVSFQNALGIPLAGSCFLEAGDLTFQGNHAKLAFINAGSSATVASTAADKNL 120
 QY 118 TFIGFSSLSFIASPGSSIT-TGKGAVSCSTGSLSTKNVSLFKNFSTDRGGAITAKTL 176
 Db 121 LFNDFSRLSIISCPSSLISPTGQCALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINKNF 179
 QY 177 SLTGTTMSALPSENT--SSKKGAIQISDALTITGNQGEVFSFSDTSSDGAIFTEASV 234
 Db 180 LLSGTQSOFASFSRQAFTKQGVVYATGTTIENSPIGVFSQNLAKSGSGALYSTONC 239
 QY 235 TISNNAKVSFIDNKVTGASSSTTGDMGGALCAVKTSTDTKVTLTGTGNOMLFSNNSTTTA 294
 Db 240 SITDNFQVIFDGNANWAAQA-----QGALICC--TTTDKVTLTGNKNLSFTNTALTY 292
 QY 295 GGAIYVKKLELASGGLTLFSRNSVNGTAPK--GGAIADSDSGELSLGADSDIVFLGNT 352
 Db 293 GGAISGLKVSISAGGPTLFQSN-ISGSAGQGGGAINIASAGELALSATSGDITFNNQ 351
 QY 353 VTSITPGTNRSSIDLGTSAKMTALRSAGRAIYFYDPTTTCGSTTFTVTLVKVNETPADSA 412
 Db 352 VTNGSTST-RNAINIIDTAKVTSIRATGQSIYFYDPTNPFTAASTDTNLNLADANSE 410
 QY 413 LOYTGNIIFTGKELSETEAADSKNLTKLQPVLTLSGGTSLSKHGVTLTQTAFTQOADS 472
 Db 411 IEYGAIVFSEKLSPTKAIANVTIRQPAVLARGDLVLDGVTTFKDLTQPSGR 470
 QY 473 LEMDVGTTLPEADTS-TINNIVINISSIDGAKKAKIETKATSKNLTLSGTTILLDPGTGP 531
 Db 471 ILMDDGTTLSAKEANLSLGLAVNLSSUDGTNKAALKTEAADKNLSLGTIALIDTEGSF 530
 QY 532 YENHSLRNPQSDIILELK---ASGTVISTATVPPIGKEKHYGQGTWGPVWGTGAST 588
 Db 531 YENHLSASTYPLLELTGTAGANGTITLALSTLTLOPEPTHYGYQGNW-QLSWANATSS 589
 QY 589 -TATFNWTKTYIPNPERIGSLVPSNLWNADFIDISSLHVMETANEGLQGDRAPWCAGIS 647
 Db 590 KIGSINWTRTYIISPERKSNPLNSLWGNFIDISINQLIETKSSGFFERELWSGIA 649
 QY 648 NFFKDSKTKTRGFRHLSGGYVIGNLHTCSKILSAAFQCLFGDRDRIYFVAKNGOTVYG 707
 Db 650 NFFYRDSMPTRHGRHISGVALGITTATPAEDQLTFAFCQLFARDRNHITGKNHGTYG 709
 QY 708 GTLYYQHNETYISLPCKL-----RPCSLSVYPTIPLVLSGNLSYTHDNLKTKYTY 761
 Db 710 ASLYPHHTTEGLFDIANFLWGRKATPAWVLSISQIIPUSFADAKFSYLTHDNLHMKTYTDN 769
 QY 762 PTVKSGWGNDSFALEFGGRAPICLDESALFEQYMPFMKLQFYVAHQEGFKQGTBARBFG 821
 Db 770 SIIRKSWENDAFCADLGASLPFVSVYLLKEVEFVKVQIYIAHQDQFYERYAEGRAF 829
 QY 822 SSRLVNALPTGIRPKESDCODATYNTLTGTVDLVRSNPDCTTTLRISGDSWTKFTGN 881
 Db 830 KSELINVEIPIGVTIFERDSKSEKGYDLTLMYILDAYRRNPKCQSLTIASDANMAYGTN 889
 QY 882 LARQALVLRAGNHCFNSNFEAFSOFSELRGSSNNVNDLGAKYQF 928
 Db 890 LARQGSVRAANHFOVNPHEMIFGQFAFEVSSSRNNTNLGSKFCF 936
 RESULT 4
 ID PMP8_CHLPN
 ID PMP8_CHLPN STANDARD; PRT; 930 AA.
 AC Q9Z393; Q9RB66;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
 DE protein 8) (Outer membrane protein 11).

GN PMP8 OR OMP11 OR CPN0446 OR CP0307 OR CPB0463.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
 OX NCBI_TaxID=83538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10519856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RT role in immunopathogenicity";
 RL Am. Heart J. 138:S491-S495(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=101923388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.P.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWI029 from USA";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW-183;
 RX Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
 RT other Chlamydia strains based on whole genome sequence analysis";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC
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 CC
 CC EMBL; A7133034; CAB37068.1; -
 CC EMBL; AB001627; AD18590.1; -
 CC EMBL; AB002193; AAF38164.1; -
 CC EMBL; AF002546; BAA98654.1; -
 CC EMBL; AB017158; AAP98394.1; -
 CC PIR; A81591; A81591.
 CC PIR; D72078; D72078.
 CC PHCI-2DPAGE; Q92393; -
 CC TIGR; CP0307; -
 CC InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR005546; Autotransporter.

DR InterPro; IPR003368; Chlamydia_PMP.
 DR Pfam; PF03797; Autotransporter_1.
 DR Pfam; PF02415; Chlamydia_PMP; 2.
 DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 930 PROBABLE OUTER MEMBRANE PROTEIN PMP8.
 FT VARIANT 177 177 T->A (in strains AR39, J138 and
 FT TW-183).
 SQ SEQUENCE 930 AA; 97669 MW; 46A9B5E3BB913C4C CRC64;
 Query Match 40.6%; Score 1936; DB 1; Length 930;
 Best Local Similarity 43.5%; Pred. No. 1.4e-97;
 Matches 415; Conservative 165; Mismatches 325; Indels 48; Gaps 17;
 QY 1 MKSSPEKPFVSTFAIPFLSM-IAT---ETVLSSASFSGNKGNGFVSRSQEDAGTYYLF 56
 Db 1 MKIPLHKLISSTLVTPILLSIATYGADASLSPTDSFDGAGGSTFTPKSTADANGTNYVL 60
 QY 57 KGNVLENIPTGTALTAKSCFNNTKGDLPFTNGNSLLFQTVDAGTVAGAAVNSVVDKS 116
 Db 61 SGNVYI-NDAGRGTAITGCCFTETTGDLTFTGKGYSFNTVDAGSNAGAAA-STTADKA 118
 QY 117 TTFIGPSSLSFIASPGSSITTTGKGAVSCSTGSLSTKNVSLFLSKNFSTD---NGGAITA 173
 Db 119 LFTGFNSLSFIAPGTTVASGKSLT-SAGALNLTGDTGTLFSSQVNSNEANNNGAITT 177
 QY 174 KTLSTLGTMTSMALFSBNTSSKGGAIQTSDALITGNQGEVSFSDNTSSDGAIFTEAS 233
 Db 178 KTLISISNTSSITFTSNAKGLGAIYSSAAASISGNTGQVFMNKGTTGGGALGFAS 237
 QY 234 VIISNNAKVSFDNKKVTGASSSTTGDMSCGAICAYKTSTDTKVLITGNQMLFSNNTSTT 293
 Db 238 SSIQTNSLSFFSGNTATDAAG-----KGGAIYCEKTGETPTLTITSGNKSLETPAENS 291
 QY 294 AGGAIYVKKLELASGGLTTLFNRNVNGTAPKGAIAIEDSGELSLSDSGDVIPLGNTV 353
 Db 292 QGGAICAGGLDLSAAGPTLFSNNRCNTAAGKGAIAIADSGSLSSANOGDTIFLGNTL 351
 QY 354 TSTT-PGTRNSIDLGTSAKMTALRSAGRAIYFYDPI---TTGSSSTTTVDVLKVNTPA 409
 Db 352 TSTSAPTSTRNAIYLGSSAKITNLRAAQGSIYFYDPIASNTTGA---DVLITNQPD 407
 QY 410 DSNALQVTGNIITGEXLSETEADSKNLTSKLLOPVTLSGCTLSLKHGVTIQATQQA 469
 Db 408 NGPLDYSGTIVFSGEXLSADEAKADNFTSLKQPLALASGTLAKGNVELDVGFTQTE 467
 QY 470 DSRLEMDVGTLEPADTSTIN--NLVINSSIDGAKKAKTETKATSKNLTSGTITLLDP 527
 Db 468 GSTLLMQPTGLK-ADTEALSLTKLVVDLSALEGKSVSIETAGANKTITLTSPLVFQDS 526
 QY 528 TGTFFENHSLRNPQSYDILELKAS-----GVTSTAVTPDPIMGKPHYGYQGTWG 578
 Db 527 SGNFYESHNTINQATPLVVFVTAATAASDIYDALLTSPVQTEP-----HYGYQHW 580
 QY 579 PIWGTGASTTATFNWTKGYIPNBERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGD 638
 Db 581 ATWADTSTAKSGTMTVTTTGYNPNERRASVVPDLSLWASFTDITRTQQIMSOANSIYQ 640
 QY 639 RAFPWAGLNFPHKOSTKTRRGHLSGGYVIGNLHTCSDKILSAAFCQLFGDRDYFV 698
 Db 641 RGLWASGTANFPHKXSGTNOAFRHKSYGYIYVGGSAEDFSENI FSVAFQQLFGKDKDLFI 700
 QY 699 AKNQGTVYGGTLYYQHNETYIISLPCKLRPC--SLSYVPTTEIPVLFSGNLSYTHTDNCLKT 756
 Db 701 VENTSHNVLASLYLQHRFLGGLP---MPSFGSITDMLKDIPLILNAQLSYSYTKNDMDT 757
 QY 757 KYTTPYTVKSGWNGDSFALEFGGRAPICL-DSALFEQYMPFMKLOFYVAHQEGFEQGT 815
 Db 758 RYTSYPEAQGSWTNNSGALEGLSLALYLPKEAPFFQGYFFFLKFOAVYRQONFKESGA 817
 QY 816 EAREFGSSRLVNLALPIGIRFDKESDQDATYNTLIGYTVDLVRSNPDCDTTTLIRISGDSW 875

Db 818 BARAPDDGDLVNCSPVGRLEKISEDEKNFPEISLAYIGDVYRKNPRSTSLMWSGASW 877
 Qy 876 KTFGTNTLAROALVLRAGNHFCNSNFQSPFELRGSSRNYYNDLGAQYOF 928
 Db 878 TSLCKNLARQAFASAGSHLTLSPHVELSGEAYELRGAHYNVDCGRYSF 930

RESULT 5

PM11_CHLPN
 ID PM11_CHLPN STANDARD; PRT; 928 AA.
 AC O86164; Q9K299;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable outer membrane protein pmpl1 precursor (Polymorphic membrane protein 11) (Outer membrane protein 4).
 GN PM11 OR OMP4 OR CPN0449 OR CP0302 OR CPB0468.
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CW1029/VR-1310;
 RX MEDLINE=99081766; PubMed=9864239;
 RA Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;
 RT "Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae";
 RL Infect. Immun. 67:375-383(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VR1310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity";
 RL Am. Heart J. 138:S491-S495(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CW1029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";
 RL Nat. Genet. 21:385-389(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CW1029 from USA";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW-183;
 RX Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
 RA Schneider S., Pohl T., Bessig A., Marre R., Melchers K.;
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with

RT other Chlamydia strains based on whole genome sequence analysis.";
 RL !- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
 CC (Potential).
 CC !- SIMILARITY: Belongs to the PMP outer membrane protein family.
 CC
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 CC
 DR EMBL; AJ001311; CA04672.1; -
 DR EMBL; AJ133034; CAB37072.1; -
 DR EMBL; AE001628; AAD18593.1; -
 DR EMBL; AE002192; AAF38159.1; ALT_INIT.
 DR EMBL; AP002546; BAA98658.1; -
 DR EMBL; AE017158; AAP98399.1; -
 DR PIR; D72077; D72077.
 DR PIR; H86546; H86546.
 DR PHCI-2DPAGE; O86164; -
 DR TIGR; CP0302; -
 DR InterPro; IPR003368; Chlamydia_PMP.
 DR InterPro; IPR000437; Prok_lipoprot.S.
 DR Pfam; PF02415; Chlamydia_PMP; 2.
 DR TIGRFAMs; TIGR01376; POMP repeat; 6.
 KW Outer membrane; Signal; Multigene family; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 928 PROBABLE OUTER MEMBRANE PROTEIN PMP11.
 SQ SEQUENCE 928 AA; 98903 MW; 788BCDD62C911402 CRC64;
 Query Match 38.9%; Score 1855; DB 1; Length 928;
 Best Local Similarity 42.7%; Pred. No. 3.3e-93;
 Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;
 QY 1 MKSPPKFFVSTFAIPP--LSMIATETVLDSSASFDGN-KNGNFVRSQEDAGTYYLPK 57
 Db 1 MKTSPVWLVSFLAFSCHLOSLANEELLSPDPSFNGNIDSGTFPKTS---ATTYSIT 56
 QY 58 GNVTLNTPGTCTAITKSCFNNTKGLPTFGNGNLLFTQVDAGTVAGAAVNSVVDKST 117
 Db 57 GNVFYFE-PKGKTPLSDCFKQTNDNLFLNGHSLTFGFDAGTHAGAAA-STTAKNL 114
 QY 118 TPIGFSSLSFTASPGSSITTKGAVSCSTGSLSTKYNLSLPSKNSFNDNGCAITAKTUS 177
 Db 115 TFGFSLLSFDSPSTTWTGQTLG-SAGGVNLENIRKLVVAGNFSTADGGAIGASFL 173
 QY 178 LTGTTMSALFSENTSSKKGAIQTSDAITITGNQGEVSFSDNTSSDGAATFEASVTIS 237
 Db 174 LTGTSGLALFNNSSSTKGAIAATTAGARIANNNTGYVRFSLNIASTSGAIDDEGTSILS 233
 QY 238 NNAKYVSFDNKVTGASSSTTGDMSGGALCAVKTSDTKVLTGNQMLFSNNSTTTAGGA 297
 Db 234 NKKFYLF-----EGNAAKT---GGAICNTKASGPELISNNKTLIPASNAETSGGA 284
 QY 298 IYVKKLELASGGLTLFSRNSVNGGTAPKGGATAIEDSGELSDSADSGDIFLGNTVTST- 356
 Db 285 IHAKKALSSGGFTFELNNVSSAT-PKGGALSIDASGELSASATGNITFVRNLTITTG 343
 QY 357 -TPGNNRISIDLGTSAKMTALRSAAAGRAIFYVDPTITTSSTTVTVLVKNETPPASALOY 415
 Db 344 STDTPKRNAINIGSNKGTTELRAAKNHNIFFFDPTIT--SEGTSSTVLLKNNINGSAGALNPF 401
 QY 416 TGN11FTCEKLSETEAAADSKNLTSLKLOPVTLSGGTFLSKHGVTLTQOATQOASRLBM 475
 Db 402 QGTILFSGETITPADELKVDADNLKSSFTQPVLSGGKLLKQKGVTLSTFSFSGEAGSLGM 461
 QY 476 DVGTTLE-PADSTTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTITLLDPTGFYEN 534
 Db 462 DSGTTLSTTAGSITITNLGINVDLSGLQPVSLTAKGASNKVIVSGKLNLIIDIEGNIVS 521

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QY 535 HSLRNPQSDIILELKASGTWTS-----TAVTPDPMGEKHEHYGQGTGPIVMTGASTT- 589
DB 522 HMFSDQLSLLKLTVDADVDTNVDISSLIPVPAEDPNSEYGFQGGWN-VNWTDTATNT 580
QY 590 --ATFNWTKGYIPNPERIGSLVPSNLNAPIDISSHLVLMETANEGLOQDRAPWCAGLS 647
DB 581 KEATATWTKGTGFPSPERKSALVNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVSSMT 640
QY 648 NFPHKDKSTKRGFRHLSCGYVITGMLHSCDKILSAACQLGRDRDYFVAKNGQTVVG 707
DB 641 NFLHKTGDNRRKGRFRTSGYVIGGSAHTPKDOLFTFAFCHLPARDKOCFIAHNSRTYG 700
QY 708 GLTYQHNET-----YISL-PCMLRPCSLSYVTEIPVLFSGNLSYTHTDNLKTKYTV 761
DB 701 GTLFFKHSHTLQPNYLRGLRAKESSEAIKFPREIPLALDVQVSFSDNRNMEHTYTSL 760
QY 762 PTVKSGWGNDSFALEFGGRAPICL-DESALFEQYMPFMKLQFYVAHQBFKEGQTEARBF 820
DB 761 PESEGSWSNECIAGGIGLDLPFLVLSNPHLPFKTFIPQMKVEMVYVQNSFFESSDGRGF 820
QY 821 GSSRLVNLALPIGIREDKESDQDA-TYNLTIGYTVDLVRSNPDCTTTLRISDSWKTGF 879
DB 821 STGRLLNLSPVGAKE-VOGDIGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPDWKIRG 879
QY 880 TNLARQALVLRAGNHCFNFSNFEAFSQFSELRGSSRNYNVDLGAQYQF 928
DB 880 GNLSRQAFLLRGSNNVYNSNCELFGHYAMELRGSSRNYNVDGTXLRF 928

RESULT 6
PMP2_CHLPN
ID PMP2_CHLPN STANDARD; PRT; 841 AA.
AC Q9Z3A1; Q9BB73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable outer membrane protein pmp2 precursor (Polymorphic membrane
protein 2) (Outer membrane protein 7)
GN PMP2 OR OMP7 OR CPN0013 OR CP0761 OR CPB0015/CPB0016.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
role in immunopathogenicity.";
RL Am. Heart J. 138:8491-8495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP SEQUENCE FROM N.A.

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RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RX Geng M.M., Schumacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
(potential).
CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
CC -!- CAUTION: Ref.4 and Ref.5 sequences differ from that shown due to a
frameshift in position 673.
CC -----
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CC -----
CC EMBL; AJ133035; CAB37083.1; -
DR EMBL; AE001586; AAD18172.1; -
DR EMBL; AE002235; AAF38561.1; -
DR EMBL; AF002545; BAA98223.1; ALT_FRAME.
DR EMBL; AE017157; AAP97948.1; ALT_FRAME.
DR EMBL; AE017157; AAP97948.1; ALT_FRAME.
DR PIR; E72130; E72130.
DR PHCI-2DPAGE; O9Z3A1; -
DR TIGR; CF0761; -
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 3.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 841 PROBABLE OUTER MEMBRANE PROTEIN PMP2.
FT CONFLICT 784 784 N -> S (IN REF.4).
FT SEQUENCE 841 AA; 89600 MW; 9064D0D0678D24C CRC64;
Query Match 32.9%; Score 1573; DB 1; Length 841;
Best Local Similarity 39.4%; Pred. No. 5.6e-78;
Matches 371; Conservative 121; Mismatches 310; Indels 140; Gaps 20;
QY 12 TFAIPPLSMIATETVLDSSASFDG-NKGNFVSRESQEDAGTYYLPKGNVTLENIPGTGT 70
DB 15 TLSSMNLGAATTELSASNFDGTTSTTSFSSKTSATDGTNYVFKDSVVIENVEKTGE 74
QY 71 ALTKECFNN--TKGDLTFGTGNSLLFQVVDAGTVAGAAVNSVVDKSTFTTGFSSLSFI 128
DB 75 TQSTSCFRNDAAGDLNFLGGGFSFTFESNIDATTAGAAIGSEAAKNTVTLGFSALSFL 134
QY 129 ASFGSITTKGAVSCSTGSLSLTKNVSLLFSKFNSTDNNGAITAKTLTLTGTTMSALFS 188
DB 135 KSPASTVTNGLGAINVK-GNLSLLDNDKVLQDNFTGDDGAINC----- 178
QY 189 ENTSKKGGAIQTSDALITITNQGEVSFSDNTSDSGAAIFTEASVTISNNAKVGFIDNK 248
DB 179 -----AGSLKIANNKSLFSI--- 193
QY 249 VTGASSITGDMGGGAI CAYKTSBTKVTLTGQMLLSNNTSTTAGGIYVKKLELAGS 308
DB 194 -----GNSSTRGGAHTKNTLTSSG 214
QY 309 GLTLFERNVNGGTAP-----KGAIAIEDSGELSLSDSGDIVFLGNTVTSPTGT-NRS 363

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Db 215 GETLF-----QGNTPAAGKGAIAIADSGTSLISGSDGDIIFEGNVTIGAT--GTVSHS 267
Qy 364 SIDLGTSAKMTALRSAGRAIFYDPIITGSSITVDVLKVNETPADSALQVITGNIIFTG 423
Db 268 AIDLGTSKIITLRAAQGHIIYFDPITVTCSTSVADALINSPDTGDKNEYTGTVFSG 327
Qy 424 EKLSETEAADSKNLTSKLLQPVTLGGTSLSKHGVTLOTQTAFTQOADSRLQVLEMDVGTTLLEP 483
Db 328 EKLSETEAADSKNLTSKLLQPVTLGGTSLSKHGVTLOTQTAFTQOADSRLQVLEMDVGTTLLEP 483
Qy 484 ADTSTI--NLVINISSDGAKAKIEFKATSKNLTLSGTTITLLDPTCTFEVNHSLRPQ 541
Db 387 ANTESIELTNLEINIDSUNGKIKLSAATAQKDIRDPVVLALSDESFYONGFLNEDH 446
Qy 542 SYD-ILELKASGTVTSTAVTDPDMGEKPHYGYQGTWGPVVGCTGASTATFNTWTKGYI 600
Db 447 SYDILELDAGKDIVISADRS--IDAVSPGYQKQW-TINWSTD-DKKAIVSWAKQSPN 503
Qy 601 PNPERIGSLVNSLWNAFIDISSHLHMETANEGLOGDRAFCWAGLSNFFHKDSTKTRRG 660
Db 504 PTAEOEAPLVNLLWGSFIDVRSFQNFTELGTGEGAPYEKREFWAGISVNLHRSRGRENQK 563
Qy 661 FRLHSGGVVIGNLTCSDKILSAFCOLFGDRDYFVAKQGTGVTGTLVYOHNETYIS 720
Db 564 FRHVSAGGAVGASTMPGGDTLSLGAQLFARDKDYFMWNTFAKTYAGSLRLQHDASLYS 623
Qy 721 LPC-----KLKPCSLSVPTPIVLFSGNLSYTHTDNDLTKY-----TTPVTKGSWG 769
Db 624 VVSILLGEGGLREILLPVSKTLPSCSYGQSLSYGHTDHMKTESLPPPPPTLSTDHTSWG 683
Qy 770 NDSFALEPGGRAPICLDSEA---LFEQYMPFMKLQFVVAHQGGFKQGTTEAREFGSSRLV 826
Db 684 GYVWAGELGTR--VAVENTSGRGFFQETPFVVKQAVYARQDSFVELGAISRDFSDSHLY 741
Qy 827 NLALPIGIRFKEQSCQDATNLTLYGVTVDLVRSNPDCTTLTIRISGDSKTRFGTLARQA 886
Db 742 NLALPIGIRFKEQSCQDATNLTLYGVTVDLVRSNPDCTTLTIRISGDSKTRFGTLARQA 799
Qy 887 LVLRAHGFNFNSFEAFSOFSEFELGRSRRNTNVDLGAKYQF 928
Db 800 GIVQASGFRSLGAAELGNFGFWRGSSRSYNVDAGSKIKF 841

RESULT 7
ID PMP6 CHLEN STANDARD; PRT; 1276 AA.
AC Q9Z899; O9JRW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable outer membrane protein pmp6 precursor (Polymorphic membrane protein 6).
DE PMP6 OR CPN0444 OR CP0309 OR CPB0460.
OS Chlamydia pneumoniae (Chlamydia phila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phila.
OX NCBI_TaxID=83358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Pan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
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RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi P., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
Schneider S., Pohl T., Essig A., Marre K., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Cell wall surface (elementary bodies (Potential)).
CC -! SIMILARITY: Belongs to the PMP outer membrane protein family.
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CC EMBL; AE001627; AAD18588.1; -
DR EMBL; AE001627; AAD18588.1; -
CC EMBL; AP002546; BAA98652.1; -
DR EMBL; AP002546; BAA98652.1; -
CC EMBL; AE017158; AAP98391.1; -
DR EMBL; AE017158; AAP98391.1; -
CC PIR; B72078; B72078.
DR PIR; B72078; B72078.
CC PIR; B86546; B86546.
DR PIR; B86546; B86546.
CC PIR; C81591; C81591.
DR PIR; C81591; C81591.
CC PHCI-2DPAGE; Q9Z899; -
DR PHCI-2DPAGE; Q9Z899; -
CC TIGR; CP0309; -
DR TIGR; CP0309; -
CC InterPro; IPR006315; Autotransport.
DR InterPro; IPR006315; Autotransport.
CC Pfam; PF02415; Chlamydia_PMP; 2.
DR Pfam; PF02415; Chlamydia_PMP; 2.
CC TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
CC Outer membrane; Signal; Multigene family; Complete proteome.
KW SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 1276 PROBABLE OUTER MEMBRANE PROTEIN PMP6.
FT CONFLICT 421 421 E -> EGGGALLAFIDSGVSDKTLGSIANNQVSLTNSA
ATVGGGAIYATKCTLTGNGSLTFDNGTNGTSGGALITETED
FTLGTGTGTVFTSTAKTGKALYSGKNNLSGNTNLLFSG
NKATGPNSSANQE (IN REF. 1 AND 4).
FT SEQUENCE 1276 AA; 132127 MW; C97FA0662C8E0B CRC64;
SQ
Query Match 30.2%; Score 1444; DB 1; Length 1276;
Best Local Similarity 29.5%; Pred. No. 9,9e-71;
Matches 382; Conservative 157; Mismatches 370; Indels 386; Gaps 26;
Qy 1 MKSFPKVFSTFAIFPL-SMIATETVLDSSASFQGNKNG--FSVRESQEDAGTITLFPK 57
Db 1 MKYSLPWLITSSALVFSLHPLMAANTDLSNDSYENGSSGAFTAKETSDASGITLIT 60
Qy 58 GNVLTLENIPGTGTATIT--KSCFNNTKGLDFTGNGSNLLFTVDAGTVAGAAVNSVVD 114
Db 61 SDVSIITNV----SAITPADKSCFTNTGGALSPVGDHSLVLQTI-ALTHDGAANNNT--N 113
Qy 115 KSTTFIGRSSLSFIASPGSSITGCGAVSCST----GSLTKNVLKSLFKNFTDNGGA 170
Db 114 TALSPFGSSLLIDSAPATGTSGGGKAI--CVNTTEGGTATFTDNASVTLQKNTSEKDGAA 172
Qy 171 ITAKTSLTGTMTSALFSENTSSKKGKAIQTSDALITTCNQGEVFSFSDNTSSDGAIF-- 229
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Db 173 VSAYSIDLAKTTAAALLDQNTSTKNGALCSTANTTTVQNSGTVTFSSNTATDKGGIYS 232
QY 230 -----TEASVTISNNAKVSFIDNKTG-ASSSTTGDM 260
Db 233 KKKDSTLDANTGVVTFKSNKTAKTGGAWSSDDNLALTGNTQVLQENKTTGSAQAANNPEG 292
QY 261 SGGAICAY-KTSTD-----TKVLTGNQMLLFSNNTS 291
Db 293 CGGAICCYLATADTKGLAISQNEQMSFTSNTTANGGAIYATKCTLDGNTLTFFQNTA 352
QY 292 T----- 292
Db 353 TAGCGGAIYETEDFSLKSGTGTVFTSTNTAKTGGALYKGNSSLTGNNTLLPSGNKATG 412
QY 293 ----- 292
Db 413 PNSSANQCGCGAIIASFLESASVTKGLIWBEDNENSVLSGNTATVSGAIYATKCALH 472
QY 293 ----- 292
Db 473 GNTLTTFDGNATAAGAIYETEDFTLTGSGTGTVFTSTNTAKTGGALHTKGNSTFKNK 532
QY 293 ----- 292
Db 533 ALVFSGNSATATATTTTQCGCGALLCNISESDIATKSLTLTENESLGFINNNTAKRSG 592
QY 293 -----TAGAIYVKKLELASGLTLFNSVNGGTAPKGGAI 329
Db 593 GIYAPKCVISGESINFDGNTAETSGAIYSKNLSITANGPVSTFNN--GG--KGGAI 647
QY 330 AIEDSGELSDSGSDIVFLGNVTSTTPTGTRSSIDLGTSAKMTALRGAAGRAIYFYDP 389
Db 648 YIADSGELSLAIDGDIETSGNEATGTTSTPN--SHLGGAKITKLAAPGHTIYFYDP 705
QY 390 IT---TGSSTTVTD-----VLKVNETPADSALQYNTGNIIFTGEXL 426
Db 706 ITWEAPASGCTIEELVINPVKAIVPPQPKNGPIASVPVVPVAPANPNTGTITVFSGKL 765
QY 427 SETEADSNLNLKLOPVLTSGLTSLKHGVTLQTAFTQOADSLEMDVGTLPADT 486
Db 766 PSODASIPANTTILNOKINLAGNVVLKEGATLQVYSFTQQPDSTVFMWDAGTLETTT 825
QY 487 ST-----INNVLINISDIDGAKKAKIETKATSKNLTLTSGTITLLDPTGTFYENHSLRNP 540
Db 826 NNTDGSIDLKNSVNLDAIDGKEMITAVNSTSGGLKISGDLKFNHNSGYFNDPGLKAN 885
QY 541 QSYDILELKA-SGTVTSTAVTPDPMGEKPHYGYQTWG--PIVWGTGASTTATFNWTKT 597
Db 886 LNLPLDLSTSGTNLDDFNPTPSSMAAPDYGQGSWTLVPKV-GAGGKVTLVAEQAL 944
QY 598 GYIPNERIGSLVPSLWNAFIDISLHYLMETANESLQDRAFCWAGLSNPFHKDSTKT 657
Db 945 GYTPKPELRATLVPSLWNAVNIHQEIAFAMSDAPSHPGIWTGGTGNAPFHODKQE 1004
QY 658 RRGFRHLSGGYVIGGNLHCTSKILSAACQLPGRDRDYFAVKNQGTGYGTLIYQHNET 717
Db 1005 NAGFRILSRGIVGGSWTTPQETFAVAFSQLFKSKDYVSDIKQVYAGSLCAQ-SSY 1063
QY 718 YISLPCKLRPCSLSYV-----PTPIPLVPSGNLSYTHTDNDLTKYTYTPYVKGSGWNSDF 773
Db 1064 VIPLHSLRRHLVKLPELPGETPLVLHGQVSYGRNHNMTTKLANNTQKGSDDWDSHF 1123
QY 774 ALFFGGRAPICLDSEALFQYMPFMKLOFYAHOEGFKQGTAREFGSRLVNLALPTG 833
Db 1124 AVEVGSLPVDLNYRL-TSYSPYKLVQVSVNKGQFQVEAADPRIFDASHLVNVSIPMG 1182
QY 834 IRFDKESDCQATYNTLTGYTDLVRSNPDCTTLTISGDSMKTFFGNLARQALVLRAGN 893
Db 1183 LTFKHESAKPPSALLTLGVAVDAYDRHPHCLTSL-TNGTSWSTFATNLRSQAFPAEASG 1241
QY 894 HFCNENFAFQSFELRGSSRNYNVDLGAQYOF 928
Db 1242 HLKLLHGLDCFASGSCELRSSRSYNANCGRYSF 1276

RESULT 8
PMP1_CHLPN
ID PMP1_CHLPN STANDARD; PRT; 922 AA.
AC Q9ZG5; Q9KIY9; Q9Z4H9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable outer membrane protein pmp1 precursor (Polymorphic membrane protein 1) (Outer membrane protein 6).
GN PMP1 OR OMP6 OR CPN0005 OR CP0770 OR CPB0006.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007504; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity";
RL Am. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=9920606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomics of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-399(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
RA Linher C., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Bisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shitai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RX Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (Potential).
CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
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CC

[illegible]

RESULT 12	PMPI	CHLMU	STANDARD;	PRT;	867 AA.
AC	Q9PL41;				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Probable outer membrane protein pmpl precursor (Polymorphic membrane protein 1).				
DE	PMPI	OR TC0267.			
GN	PMPI	OR TC0267.			
OS	Chlamydia muridarum.				
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.				
OX	NCBI_TaxID=83560;				
RI	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MoPn / Nigg;				
RX	MEDLINE=20150255; PubMed=10684935;				
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bowan C., Dodson R., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Winn M., Nelson M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;				
RA	Eisen J., Fraser C.M.;				
RT	"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";				
RT	Nucleic Acids Res. 28:1397-1406(2000).				
RL	-!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (Potential).				
CC	-!- SIMILARITY: Belongs to the PMP outer membrane protein family.				
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CC	EMBL; AEO02294; AAF39136.1; -;				
DR	PIR; F81721; F81721.				
DR	TIGR; TC0267; -;				
DR	InterPro; IPR003368; Chlamydia_PMP.				
DR	Protein; PF02415; Chlamydia_PMP; 1.				
DR	TIGRFAMs; TIGR01376; POMP repeat; 6.				
KW	Outer membrane; Signal; Multigene family; Complete proteome.				
FT	SIGNAL	1	POTENTIAL.		
FT	CHAIN	30	867	PROBABLE OUTER MEMBRANE PROTEIN PMPI.	
SQ	SEQUENCE	867 AA;	95017 MW;	557994185A9E5652 CRC64;	
Query Match					
Best Local Similarity 29.5%; Pred. No. 4.5e-42;					
Matches 281; Conservative 144; Mismatches 384; Indels 144; Gaps 30;					
Qy	17	PLSMIATETVLDSSASFDGNKG-----NFS---VRESQED-----AGTYLF	56		
Db	18	FTALIFGQDALDKSALITKPNISIVCTFEDCWNENFSPALLSHARQDDPLYIIGNTH--	75		
Qy	57	KGNVTLLENI--PGTGTATITKSCFNNTKLTFTGNSLLFTQDAGTVGAAGVNSVVDK	115		
Db	76	--NWFVSNLEPST-----NEERFLKEKGDLSI-----Q	101		
Qy	116	STTFPGFSSLSFIASPGSSITTKGAVSCSTGSLSTKNVSLFSKNFSTNGGAITAKT	175		
Db	102	DFRFLSPDCCSSTEDSPSLVHK-----NQQLFLRNNNGMSFYRHNHSGSGGALSTDA	155		
Qy	176	LSLTGTTMSALFSENTSSKKGAIQTSDALTITGNQGEVSFSDNTSSDGAALFTASVT	235		
Db	156	LFLQHNLYLFTNFENSACKNGGAIQ--AQTLSLRNVSSLSFSRRNLANGGAICCQNLC	214		
Qy	236	ISNNAKVSEIDNKVTGASSTTGDMSGGALCAVYKTSIDTK--VTLTGNQMLLFSNNTST	292		
Db	215	SGNVNPLFFTTNSA-----LNGGALCCINQNLSEKGLCSLAYNQETLFGNSAK	264		
Qy	293	TAGGAIYVKKLELASGGLTILFSNSVNGGTAPKGGAIADSDGSLSDASDGSDIVFLGNT	352		

Db 265 EKGAIYTKHMLRHNGPVSFWNS-----AKLGAIAIQSGSLIIAGGSLVLFQNS 319
Qy 353 VTSPTGNNRSSIDLTGSAKTALESAAGRAIVFDPIITG-----SSTVTDLVKNE 406
Db 320 CHFSDQGVRAIVLEKNALLSLEARGH-DILFDPPIQVQVBPESFTSALPLRI-Q 377
Qy 407 TPADSALOYTGNIIFTGSKLSETAADSKNITSLKLPVTLGGTSLSKHGVTIQTQAPT 466
Db 378 TINTREA-----VIFSSNLSKEEKTEA-NLSKIQPIELQSGCLVKDRVILSAPSLS 430
Qy 467 QOADSRLMDVGTTLLEPADTSTINNLVINISIDGAKKAKIETKATS-KNUTLSGTITLL 525
Db 431 QAPQALLMDVGTSLTSSDLKLTLSLPLSHSIDTENSVSQSPTLSIQKIFLNS----- 486
Qy 526 DPTGTFYENHSRLNPQSDILELKAAGTSTAVTDP-PIMGEKPHYGQGTWGPVWGT 584
Db 487 -EHENFYENVELLSKQDKIDPL-----SLPKGLPHDPDLPDGNLSHFYQGDWN-FSWQT 540
Qy 595 G-ASTTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISLHYLMETANEGLQGDRAF-- 641
Db 541 SDQRETLVANWTANSYIIPHERQSALVANTLWNTYSDMQAVQSMINTTAAQ--GAYLFGT 598
Qy 642 WCAGLSNFF--HKDSTKTRRGRFHLGGYVIGGNLHTCSDKILSAFQCLFGRDRDYVA 699
Db 599 WGSVSNLFYGHGNSGKSTDNWKRSLGLFGLSTHSLDDHSHFCLAAQGLFKGSDSFT 658
Qy 700 KNQGVYGGTLYQYHNEYIYSLPCKLRPCSLSYVPTLP--VLPFGNLSYTHTDNDLKT 756
Db 659 SADTTSY-----TAAIQTQATSLIKISAQACYNESHELKT 695
Qy 757 KYTTYPTVK-GSWGNDSPALFEGGRAPICLDESALFEQYMPFMKLFQVYAHQEGFKEQT 815
Db 696 KYRSPKEGGAWHSAVVSIGSIPVNSGSLFSSFSIFSKLQFGSGQDGFESRG 755
Qy 816 EAREPGSRLVNLALPIGIRDKESDQDQATNLTGLTVDLVRNPDPCTTLIRISGDSW 875
Db 756 EAPAFADSSFTNISLVPVGAIEKSKQKTRNYHFLGAYIQDLKRCVSGPVTLLKNSVTW 815
Qy 876 KFTGNLARQALVLRAGNHFCFNSNFEAFSPFELGRSSRNYNVDLQAKYQF 928
Db 816 DAPMANLDSRAWMLTNRALH-RFQTLVNSYMLRGQSYSLDLGTTTRF 867

RESULT 13

PMPI CHLTR
ID PMPI CHLTR STANDARD; PRT; 878 AA.
AC 084882;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp1 precursor (Polymorphic membrane protein 1).
DE protein 1).
CN PMPI OR CT874.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UM-3/Cx;
RX MEDLINE=93000809; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."
RT Science 282:754-759(1998).
RL -!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (Potential).
CC -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
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CC -----

DR EMBL; AB001361; AAC68472.1; -
DR PIR; B71460; B71460.
DR InterPro; IPR003368; Chlamydia PMP.
DR Pfam; PF02415; Chlamydia PMP; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 6.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 878 PROBABLE OUTER MEMBRANE PROTEIN PMPI.
SQ SEQUENCE 878 AA; 95592 MW; DF1FA31707EE48B CRC64;

Query Match 18.1%; Score 863; DB 1; Length 878;
Best Local Similarity 30.1%; Pred. No. 1.8e-39;
Matches 260; Conservative 124; Mismatches 368; Indels 112; Gaps 23;
Qy 118 TFIGFSSLSFIASPGSSITTKGAVS-----CST-----GSLSLTKN 154
Db 74 SYCFVSKLHITDPKEALFKEKGLDSIQNFRFLSFTDCSSKESPSSIHOXNGQLSLANN 133
Qy 155 VLLFSKNFSTNDGATKATLSLTGTTMSALPSENTSSKGGAIQTSDALITGNQGEV 214
Db 134 GMSFCRNHARGSGAISADAFSLQHNYLFTAFBENSCKNGGAIQ-AQTSLSENVSPI 192
Qy 215 SPSNTSDSCAAIFTESAVTISNNAKVSFDNKTGASSTTGDMSGGAIQA---YKTS 271
Db 193 SFARNRDLNGAICCSNLCISGNVNPFFTGNSAT-----NGAICCSIDLNTS 242
Qy 272 TDTKVTLTGNQMLFSSNNITSTAGGAIYVKKLELASGGLTLFSSNVSNGTAPKGAIAI 331
Db 243 EKGSLSLACNQETLFASNAKEKGAIVAKHMLRYNGPVSFINNS-----AKIGGAI 297
Qy 332 EDSGELSLSADSGDIVFLGNTVTSTPGTNRSSIDLGTSAKNTALRSAGRAIYDPI 391
Db 298 QSGGSLSLAGEGSLVLFQNSQRTSDQGLVRNAYILEKDALSLSEARNG-DILEFDP 356
Qy 392 TGSSTVTVDLVKVNTPADSALQVT-----GNLIPTGKLSSETAA 432
Db 357 QESS-----KESPLPSSLOASVSPPTATASPLVIQTSANRSVLFSSERLSEEXT 408
Qy 433 DSKNLTSLKLPVTLGGTSLSKHGVTIQTQADSRLMDVGTTLLEPADTSTINNL 492
Db 409 PD-NLTSQLOQPIELKSGRLVKDRVLSAPLSQDPQALLIMEAGTSLKTSDDLKATL 467
Qy 493 VINISSIDGAKKAKIETKATSKNLTSLGTITLLDPTGTFYENHSRLNPQSDVILELKASG 552
Db 468 SIPLHSLDTEKSVTIH-----APNLSIQKIFLNSGDNFENVELLSKEQNNIPLTUS- 522
Qy 553 TVTSTAVTPDPIMGEKPHYGQGTWGPVW---GTGASTTATFNWTKTYIPNPERIGSL 609
Db 523 KEQSHLHLPDGNLSS--HFGYQGDW-TESKDSDEGHSLIA--NWTPKNYVPHPERQSTL 577
Qy 610 VPNSLWNAFIDISLHYLMETANEGLQGDRAF--WCAGLSNFF--HKDSTKTRRGRFHL 665
Db 578 VANTLWNTYSDMQAVQSMINTIAHG--GAYLFGTWGSAVSNLFYAHDSGKPIDNWHHS 635
Qy 666 GGYVIGGNLHTCSDKILSAACQLFGRDRDYFAKNQGTVYGGTLYQYHNEYIYSLPCKL 725
Db 636 LGYLFGLSTHSLDDHSHFCLAAQGLLKGSDFSTTSTTSTIATVQAO-----LA 688
Qy 726 RPSLSYVPTPIPLVLFSGNLSYTHTDNDLTKYTTYPTVK-GSWGNDSPALFEGGRAPIC 784
Db 689 -----MKISAQACYNESIHKLTKYRSFSGKSGWHSVAVSGVCASIPV 735
Qy 785 LDESALFEQYMPFMKLFQVYAHQEGFKEQGTAREFGSRLVNLALPIGIRDKESDQD 844
Db 736 SNGSLFSSFSIFSKLQFGSGTQDGFESSGRIKRSFASFRNISLPMGITPEKSKQTR 795
Qy 845 ATYNLTGLTYVDLVRNPDCITTLIRISGDSMKTFTGNLARQALVLRAGNHFCFNSNFEAF 904

Db 796 NYYIFLGYIQLKRDVSGSPVLLKNVSWDAPMANLDSRAVMPRLTNRQALH-RLQTL 854
QY 905 SQFSFELRGSSRNYNVDLAKYQF 928
Db 855 LNVSVYLRGQSHSYSLDLGTTYRF 878

RESULT 14
PM21_CHLPN
ID PM21_CHLPN STANDARD; PRT; 1609 AA.
AC Q9Z6U5; Q9RB58;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable outer membrane protein pmp21 precursor (Polymorphic membrane protein 21).
GN PM21 OR CPN0963 OR CP0897 OR CPB1000.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RN Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehlendorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (potential).
CC -! SIMILARITY: Belongs to the PMP outer membrane protein family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE001676; AAD19099.1; -
CC EMBL; AE002248; AAF38684.1; -
CC EMBL; AP002548; BAA99171.1; -
CC

DR EMBL; AE017160; AAP98929.1; ALT_INIT.
DR PIR; A86611; A86611.
DR PIR; H72013; H72013.
DR PHCI-2DPAGE; Q9RB58; -
DR TIGR; CP0897; -
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF02415; Chlamydia_PMP; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMs; TIGR01376; POMP repeat; 13.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1609 PROBABLE OUTER MEMBRANE PROTEIN PMP21.
FT CONFLICT 420 420 I -> M (IN REF. 3).
SQ SEQUENCE 1609 AA; 170865 MW; 2604C39FC4024CB CRC64;
Query Match 14.4%; Score 685.5; DB 1; Length 1609;
Best Local Similarity 24.6%; Pred. No. 1.8e-29;
Matches 254; Conservative 144; Mismatches 372; Indels 253; Gaps 36;
QY 60 VTLENIPTGTAITKSCP--NNTKGLTFTGNSLLFQTVDA GTVAGAAVSVVDKST 117
Db 686 VSSTDIRGGGAILAQHIFITDNT-GNLFESG-----LGGGEESSTV----- 726
QY 118 TIGFSSLSFIAPGSSITTKGAVSCSTGSLTKNVLSLLFSKNPST---DNGGAIK 174
Db 727 -----GDLAIVGGAL--LSTNEVNCNQNVFSDNVTSGCSGGAILAK 771
QY 175 TLSLTGTTMSALFSENTSSKGGAI--QTSADLTITGNGEVSFSDNTSSDSGAIIPT-EA 232
Db 772 KVDIS-ANHSVEFVSGSKFGGAVCALNESVNIITDNGSAVSFKNRTLGGAGVAAPOG 830
QY 233 SVTI-SNNAKVSFDNKVTGAS-----SSTGDMSG-- 262
Db 831 SVTICGNOGNIIFAKENFVFSGENQSGGAIANSVNIQDNAGDILFVSNSTGSGYGA 890
QY 263 --CAICAYKTSTDTKVTLTGNG--MLFNSNTSTA-----GGAIYVKKLELA--S 307
Db 891 FVGSLSVASEGSPNRTLTITGNSGDI LFAKNSTQTAASLSEKDSFGGAIYQNLKIVKNA 950
QY 308 GGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPGNNRSIDL 367
Db 951 GNVSFY-----GNRAPSAGVQIADGGVCLAEFGDILFEGNI---NFDGSFNAIHL 1001
QY 368 GTSAKMTALRSAAGRIAYFYDPTTGSST---TVTDV-----LKVNETPA-DSALQY 415
Db 1002 GNDISKIVLSAVQDKNIIIFQDAITTYEENTIRGLPDKDVSPLSAPSLIFNSKPDQDSAQHH 1061
QY 416 TGNITFTGKLETERAADSKNLTSKLLQFVTLSSGGLSLKHGVTLTQTAFTQADSELEM 475
Db 1062 EGTIRFS-----RGVSKIPQIAAQEGTLASQNAELWLAGKQBTGSSIVL 1108
QY 476 DVGVTLEPADTSTINN-----LVINISSIDGAKKAKIETKATSKNLTL 519
Db 1109 SAGSILRIFDSDQVDSAPLPENKEETLVSAQVQINNSSTPNKDKAVDTPVLADIISIT 1168
QY 520 -----GTITL-----LDPTGTFYENHS-LRNPQSYDIL 546
Db 1169 VDLSSFPVQDGTLPPLPEIITPKGTLKLSNAIDLKIIDPTNVGYENHALLSHKDIPLI 1228
QY 547 ELKASCTVTSTAVTPDPIMGEKF-----YGYQGTW-----GPIVWGTGASIT 589
Db 1229 SILKTAGMTGTPTADASINIKIDVSLPSITPATYTGHTGVWSESKNMGDLRLVVG----- 1282
QY 590 ATFNWTKCYIENPERIGSLVNSLWNAIDISL-----HYLMETANEGLQGDRAFWC 643
Db 1283 -----WQPTCYKLNPEKQAGALVNLNLSHYTDLRALKQEIFAHTTIAQRMELDFSTNVWG 1337
QY 644 AGLSNFFHKDSTKTRGRFRLHSGGVYVIGNLIHTCSKILSAAPCOLFGR-DRDYFVAKN- 701
Db 1338 SGLGVVEDCQNGEFDGFKHLHTVALGLDITQLVEDFLIGGCFSGQFFGKTESQSYAKND 1397

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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:10:51 ; Search time 21 Seconds
(without alignments)
4250.749 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFFKFPVSTFAIFPLSM.....FELRGSRNVNVDLAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3991	83.6	772	2	H86492
2	2058	43.1	928	2	G86546
3	2058	43.1	928	2	G81591
4	1982	41.5	928	2	E86546
5	1982	41.5	928	2	B72077
6	1965	41.2	936	2	C72078
7	1964	41.1	936	2	C86546
8	1964	41.1	936	2	B81591
9	1940	40.6	930	2	D86546
10	1940	40.6	930	2	A81591
11	1936	40.6	928	2	D72078
12	1855	38.9	928	2	H86546
13	1855	38.9	928	2	D72077
14	1855	38.9	949	2	F81591
15	1573	32.9	841	2	E72130
16	1444	30.2	1276	2	H86546
17	1444	30.2	1276	2	C81591
18	1442.5	30.2	922	2	B72131
19	1442.5	30.2	922	2	E86491
20	1441.5	30.2	922	2	F81539
21	1383.5	29.0	1407	2	B72078
22	1377.5	28.9	973	2	H86547
23	1377.5	28.9	973	2	F72076
24	1377.5	28.9	995	2	C81593
25	1246	26.1	712	2	E86492
26	1120.5	23.5	1013	2	G71460
27	1051	22.0	987	2	H81722
28	1017.5	21.3	445	2	E86493
29	916	19.2	359	2	C86493

30	911	19.1	867	2	F81721
31	863	18.1	878	2	B71460
32	821	17.2	494	2	D86493
33	792	16.6	427	2	A86493
34	768	16.1	186	2	G86492
35	685.5	14.4	1609	2	A86611
36	685.5	14.4	1609	2	H72013
37	672.5	14.1	978	2	G72076
38	670	14.0	947	2	G86557
39	667.5	14.0	978	2	B81593
40	667.5	14.0	978	2	C86547
41	666	14.0	947	2	D72067
42	666	14.0	1723	2	H86557
43	666	14.0	1723	2	E72067
44	666	14.0	1732	2	C81601
45	665.5	13.9	946	2	C86549

ALIGNMENTS

RESULT 1

H86492

Pmp_3 [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001

C:Accession: H86492

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: H86492

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-772 <STO>

A:Cross-references: GB:BA000008; NID:g8978389; PIDN:BAA98226.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: pmp_3_2

Query Match 83.6%; Score 3991; DB 2; Length 772;
Best Local Similarity 99.9%; Pred. No. 2.3e-208;
Matches 771; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	157	LLFSKNFSTDNGGAI	TAKTALSLTGT	TMSALFSENTSSKKGAI	QTSDALITNGQEVSF	216				
Db	1	MLFSKNFSTDNGGAI	TAKTALSLTGT	TMSALFSENTSSKKGAI	QTSDALITNGQEVSF	60				
QY	217	SDMTSSDSGAAI	FTASVTI	SNNAKV	SFIDNKVTGASS	TTGDMSGGAI	CAYKTSTDTKV	276		
Db	61	SDMTSSDSGAAI	FTASVTI	SNNAKV	SFIDNKVTGASS	TTGDMSGGAI	CAYKTSTDTKV	120		
QY	277	TLTGNQMLLF	FSNNTSTAGGAI	VYKLELAGSGGLT	LFSRNSVNGGTAPKGAIAEDSGE	336				
Db	121	TLTGNQMLLF	FSNNTSTAGGAI	VYKLELAGSGGLT	LFSRNSVNGGTAPKGAIAEDSGE	180				
QY	337	LSLSADSGDI	VFLGNVT	STTTPG	TNRSSIDLGT	SAKMTALRSAGRAI	FYDPDITGSSST	396		
Db	181	LSLSADSGDI	VFLGNVT	STTTPG	TNRSSIDLGT	SAKMTALRSAGRAI	FYDPDITGSSST	240		
QY	397	TVTDVLKVN	ETPADSALQY	TGNIIFTG	EKLSSETAADS	KNLTSKLLQPVTL	SGGTL	SLKH	456	
Db	241	TVTDVLKVN	ETPADSALQY	TGNIIFTG	EKLSSETAADS	KNLTSKLLQPVTL	SGGTL	SLKH	300	
QY	457	GVTLQTA	FTQQADSR	LEMDVGT	TLEPADT	STINNLVINI	SSIDGAKK	AIETKATSKNL	516	
Db	301	GVTLQTA	FTQQADSR	LEMDVGT	TLEPADT	STINNLVINI	SSIDGAKK	AIETKATSKNL	360	
QY	517	TLSGTTIL	DDPTGTF	FYENHSLRN	PQSYDILE	KASGTVT	STAVT	PPDIMG	KEPHYQGT	576
Db	361	TLSGTTIL	DDPTGTF	FYENHSLRN	PQSYDILE	KASGTVT	STAVT	PPDIMG	KEPHYQGT	420
QY	577	WGPIVNGT	GASTTAT	TENWTKT	GYIPN	PERIGSL	VPNLWNA	FI	DISSLHYLMETANEGLQ	636

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Db 421 WGPVWGTSATATFNWTKYIENPERIGSLVPSNLWNAFIDISLHLMETANEGLQ 480
QY 637 GDRAFWCAGLSNFFHKDSTKTRGRPHLSGGVVIIGNLHLCSDKILSAACOLPGRDRDY 696
Db 481 GDRAFWCAGLSNFFHKDSTKTRGRPHLSGGVVIIGNLHLCSDKILSAACOLPGRDRDY 540
QY 697 FVAKNOGTVYGGTLYYQHNETYISLPCKLRPCSLSVPTETIIVLPSGNLSYTHTDNDLKT 756
Db 541 FVAKNOGTVYGGTLYYQHNETYISLPCKLRPCSLSVPTETIIVLPSGNLSYTHTDNDLKT 600
QY 757 KYTTYPTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLOFVYAHQSGFKEQGT 816
Db 601 KYTTYPTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLOFVYAHQSGFKEQGT 660
QY 817 ABERGSSRLVNLALPIGIRFDEKSCODATYNLTGYVDLVRSPDCTTTLIRISGDSWK 876
Db 661 ABERGSSRLVNLALPIGIRFDEKSCODATYNLTGYVDLVRSPDCTTTLIRISGDSWK 720
QY 877 TFGTNLARQALVLRAGNHCFCNSFEAFSQSFELRGSSRNYNVDLGAKYQF 928
Db 721 TFGTNLARQALVLRAGNHCFCNSFEAFSQSFELRGSSRNYNVDLGAKYQF 772

RESULT 2
G81591
polymorphic outer membrane protein G family [imported] - Chlamydomophila pneumoniae (strain
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C:Accession: G81591
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: G86546
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <STO>
A:Cross-references: GB:BA000008; NID:g8978821; PIDN:BAA98657.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_10
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match 43.1%; Score 2058; DB 2; Length 928;
Best Local Similarity 46.7%; Pred. No. 1.2e-103;
Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSPPKPFVF-STFAIF---PLSMIATETVLDSASFQGNKN-GNFSVRESQBDAGTTL 55
Db 1 MKSQFSLVLSSTLACFTSCSTVFAATAENIGPSDSFDGNTGTTPKNT--TTGIDYT 58

QY 56 FKGNTVLENIPTGTATKSCFNNTKGDLTFTGNGNSLLFQTVDACTVAGAAVNSVVDK 115
Db 59 LTGDITLQNL-GDAAALTKGCFSDTTESLFAAGKVCG-GDITFDNNGTILPKQDYCEENGGAIST 115

QY 116 STTFICGSSLSFIASPGSGITT--GKGAIVCSCTGSLSLKTNVLSLFSKPNFSTDNGGAITA 173
Db 116 NLSLTGFSLSLTLFAAPSSVITPSPGKAVKCG-GDITFDNNGTILPKQDYCEENGGAIST 174

QY 174 KTLSLGTGTMALFSNNTS---KKGAIQTSDALITITGNQGBVSFSDNTSSDSGAIFT 230
Db 175 KNLSLKNSTGSIISFEGNKSATGKGAICATGTVDTNNTAPTFLFSNNIAEAGGAINS 234

QY 231 EASVTLSNNAKVFINKYTVGASSSTTGMSSGCAICAYKTSTDTKYTLTGNOMLFSNNT 290
Db 235 TGNCCTTGNTSLVFSNSVT---ATAG--NGAL-----SGDADVTISGNQVTFSGNQ 293

QY 291 STTAGGAIYVKKLELAS--GGLTLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVF 348
Db 284 AVANGGAIYAKKLTLAGSGGGGSIFFSNIVQGTAGNGGAISILAAGECSLSAEAGDITF 343

QY 349 LGNTVSTTP-GTNRSSIDLGTSKMTALSAAGRAIFYDPTTGGSTTVTDLVKNET 407
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Db 344 NGNAIVATTPQTTKENSIDIGSTAKITNLRAISGHSIFPYDPTANTAADSTDTLNLKA 403
QY 408 PADSAALQYTGNIIFTGEKLSSETAADSKNLKSLQPVTLTSGGTLSLKHGVTLQTOAFTQ 467
Db 404 DAGNETDYSGLSVFSGEKLSEDEAKVANLSTLTQVPVTLTACNLVLRGVTLDYKGFTQ 463
QY 468 QADSLEMDVGTTLLEPA-DTSTINNLINISSIDGAKAKIETKATSKNLTLSGTTLLD 526
Db 464 TAGSSVIMDAGTTLKASTEETVLTGLSIPVDSLGBGKVVIAAASAASKNVALSGPILLD 523
QY 527 PTGTYENHSLNPSQSYDILELKASGTVTSIAVTPDPIMGEKFEHYGQGTWGPVW--- 582
Db 524 NQGNAYENHDLGKTQDFSVQLSALGTATTTDPAVPTVATPTHYGYQGTWG-MTWVDDT 582
QY 583 -GTGASTTATFNWTKYIPNERIGSLVPSNLWNAFIDISLHLMETANEGLQDRAF 641
Db 593 ASTPKTKATLAWNTGVLNPEROGPLVPSNLWGSFSDIQAIQGVIERALSATLCSDRGF 642
QY 642 WCAGLSNFFHKDSTKTRGRPHLSGGVYITGNLHLCSDKILSAACOLPGRDRDYVAKN 701
Db 643 WAAGVANFLDKDKGKKYRHKSGGYATGGAATCSENLI5FAFCQLFGSKDFLVAKN 702
QY 702 QGTVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TELPVLPFSGNLSYTHTDNDLKT 758
Db 703 HTDITAGAFYIQH---ITECSGFTGCLLDKLPGWSHKPLVLEGLAYSHVSNDLTKY 758
QY 759 TTYPTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLOFVYAHQSGFKEQTEAR 818
Db 759 TAYPEVKGSGWGNANFMWLGASSHSYPEVLHCFDIYAPYIKLNLTYIRODSSEKGTGR 818
QY 819 EFGSRLVNLALPIGIRFDEKSCODATYNLTGYVDLVRSPDCTTTLIRISGDSWKTF 878
Db 819 SFDDNSLNLSPIGVKPEKFSDCNDFSVDLTLSVVPDLIRNDPKCTTALVISGASWET 878
QY 879 GTNLARQALVLRAGNHCFCNSFEAFSQSFELRGSSRNYNVDLGAKYQF 928
Db 879 ANNLARQALQVRAGSHYAFSPMPEVLGQFVFRGSSRIYNVDLGGKQF 928

RESULT 3
G81591
polymorphic membrane protein G family CP0303 [imported] - Chlamydomophila pneumoniae (stra
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C:Accession: G81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: G81591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38160.1; PID:g7189233
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0303
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G

Query Match 43.1%; Score 2058; DB 2; Length 928;
Best Local Similarity 46.7%; Pred. No. 1.2e-103;
Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSPPKPFVF-STFAIF---PLSMIATETVLDSASFQGNKN-GNFSVRESQBDAGTTL 55
Db 1 MKSQFSLVLSSTLACFTSCSTVFAATAENIGPSDSFDGNTGTTPKNT--TTGIDYT 58

QY 56 FKGNTVLENIPTGTATKSCFNNTKGDLTFTGNGNSLLFQTVDACTVAGAAVNSVVDK 115
Db 59 LTGDITLQNL-GDAAALTKGCFSDTTESLFAAGKVCG-GDITFDNNGTILPKQDYCEENGGAIST 115

QY 116 STTFICGSSLSFIASPGSGITT--GKGAIVCSCTGSLSLKTNVLSLFSKPNFSTDNGGAITA 173
Db 116 NLSLTGFSLSLTLFAAPSSVITPSPGKAVKCG-GDITFDNNGTILPKQDYCEENGGAIST 174

QY 174 KTLSLGTGTMALFSNNTS---KKGAIQTSDALITITGNQGBVSFSDNTSSDSGAIFT 230
Db 175 KNLSLKNSTGSIISFEGNKSATGKGAICATGTVDTNNTAPTFLFSNNIAEAGGAINS 234

QY 231 EASVTLSNNAKVFINKYTVGASSSTTGMSSGCAICAYKTSTDTKYTLTGNOMLFSNNT 290
Db 235 TGNCCTTGNTSLVFSNSVT---ATAG--NGAL-----SGDADVTISGNQVTFSGNQ 293

QY 291 STTAGGAIYVKKLELAS--GGLTLFSRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVF 348
Db 284 AVANGGAIYAKKLTLAGSGGGGSIFFSNIVQGTAGNGGAISILAAGECSLSAEAGDITF 343

QY 349 LGNTVSTTP-GTNRSSIDLGTSKMTALSAAGRAIFYDPTTGGSTTVTDLVKNET 407
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RESULT 5
B72077
polymorphic membrane protein G family CP0306 [imported] - Chlamydomophila pneumoniae (strain
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: B72077; B81592
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: B72077
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: GB:AB001628; GB:AE001363; NID:G4376730; PIDN:AA018591.1; PID:G437673
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: B81592
A:Molecule type: DNA
A:Residues: 1-928 <REA>
A:Cross-references: GB:AE002192; GB:AE002161; NID:G7189226; PIDN:AAF38163.1; PID:G718923
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: pmp.9; CP0306
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G
Query Match 41.5%; Score 1982; DB 2; Length 928;
Best Local Similarity 45.2%; Pred. No. 1.5e-99;
Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;
QY 1 MKSSPPKVFSTFAIFPLSM-----IATETVLDSSASFDGKNGKNGFVSRESQEDA-GTT 53
Db 1 MKSSLHWLTLSSSLALPLSLNFAAFAVVEINLGTNSFSG--PGTYPPAGTTNADGTI 58
QY 54 YLFKGNVTLENIPTGTATKSCFNNTKGDLTFTGNGSNLLFQTVDAAGTVAGAAVNSVV 113
Db 59 YNLTDGVISITN-AGSPALTALSCFKETGTLNLSFQGHGYQLIQTNDAG--ANCTFTNTAA 115
QY 114 DKSITTFIGFSSLSFTASPGSSTTCKGAVSCSTGSLTKVNLSLLPKNSFSDNGGALTA 173
Db 116 NKLLSFGSFLSLIQT--TTATTTGAIK-STGACISQSNVSCYFGNFNDNGGALQG 172
QY 174 KTLSTGTMTGALFSENTSSKKGAIQTSDALITGNGEVSFSDNTSSDGAALFTBAS 233
Db 173 SSISLS-LNPNLTPAKNATOKGALYSTGGITINNTLNSAFSENTAANGGALYTEAS 231
QY 234 VTISNNAKVFDINKVTGASSSTTGDMGGGAIQAYKTSTDTKV-TLTGNQMLLFSNNTST 292
Db 232 SPISNKAISFTNNSVTATSA-----TCGAIYCSSTSAKPVLTLSDNGELNFTGNTAI 285
QY 293 TAGGAIYVKKLEASGGITLFSRNSVNGGTAPKCGAIAIBOSGELSLSADSGDIYFLGNT 352
Db 286 TSGGAIYTDNLVSSGGITLFPKNNIAITAPLGAIAIADSGSLSALGDDITFEPTG 345
QY 353 V---TSTTPGTRNSIDLG-TSAKMTALRSAGRAIFYDPTTITGSSSTTVTDVLKVNETP 408
Db 346 VVKGASSQTTTRNSINIGNTNAKIVQLRASQNTIIFYDPTTITTAALS DALNLNGPD 405
QY 409 ADSALQYTGNIIFTGKELSETEAASKNLTSKLQPVTLSGGTLSELKHGVTLQTAFTQQ 468
Db 406 LAGNPAYQGTIIVFSGEKLSEAAEADNLKSTIQOPLTLAGQLSLKSGVTLVAKFSQS 465
QY 469 ADSRLMDVGTTLLEPADTSTINNLVINISSIDGAKKAIETKATSKNLTLSTITLLDPT 528
Db 466 PGSTLLMDAGTTLTADGTTINNLVNDLSLKETKATLKATQASQTVTLSSGLSLVDPS 525
QY 529 GTTFYENHSLRNQSDYDILLELKAS--GTVTSTAATPDDPIINGEKFYGYQGTWGPVIWGTGA 586
Db 526 GNVYEDVSNWNPQVFSCLTTLTADDPANIHITDLAADPLEKPNHGWYQGNWA-LSWQEDT 584
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QY 587 ST---TATFNWTKGYIPNPERIGSLVPSLWNAFIDISSLHYLMETANEGLOGDRAFWC 643
Db 585 ATKSAATLTWTKGYENPERRGTAVNTLWGSFVDRSTQQLVAITVROSQETRGITWC 644
QY 644 AGLNFFHKDSTKRRGFRHLSGGVIGGNLHTCSDKILSAFACOLFGRDRDYFAVKNQG 703
Db 645 EGISNFFHKDSTKINKRFRHLSAGVVGATTLASDNLITAAFCOLFGRDRDHFINKRA 704
QY 704 TVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNLTKYTT 760
Db 705 SAYAASLHLQHLATLSS-----PSLLRYLPGSESEQPVLFDAQISYIVSKNMTKTYTQ 758
QY 761 YPTVKGWGNDSFALEFCGRAP-ICLDESALFEQMPFMKQFVYAHQEGKEQOTE-AR 818
Db 759 APKGESSWYNDGCALEASSLPTALSHSHEGLFHAYFPFIKVEASYIHQDSFKERNITLVR 818
QY 819 EFGSSRLVNALPTGIRFDKSDCQDATYNTLTGYVDLVRSDPCTTTLRISGDSWKTFF 878
Db 819 SFDGDLINVSPIGITEFRFSRNERASYEATVIYADVYRKNPDCCTTALLNNTSWKTT 878
QY 879 GTNLARQALVLRAGNHFCNSNFEAFSOFSPELRGSSRNYNVDLGAQYQF 928
Db 879 GTNLSRQAGIGKAGIFYAFSPNLEVTNLSMEIRGSSRSYNADLGCKEQF 928
RESULT 6
C72078
polymorphic outer membrane protein g family - Chlamydomophila pneumoniae (strain CWL029)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: C72078
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: C72078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-936 <ARN>
A:Cross-references: GB:AB001627; GB:AE001363; NID:G4376721; PIDN:AA018589.1; PID:G437672
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: pmp.7
C:Superfamily: Chlamydomophila pneumoniae polymorphic outer membrane protein G
Query Match 41.2%; Score 1965; DB 2; Length 936;
Best Local Similarity 43.4%; Pred. No. 1.3e-98;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;
QY 1 MKSFPKVFSTFAIF-PLSMIATETVLDSS-ASFDGKNGKNGFVSRESQE-DAGTITYLFK 57
Db 1 MKSSVSVLFFSSSIPLFSSLSIVAAEVTLDDSSNNSYDGSNGTTFVFTTDAAGTYSLL 60
QY 58 GNVLTLENIPTGTATKSCENNTKGDLTFTGNGSNLLFQTVDAAGTVAGAAVNSVVDKST 117
Db 61 SDVSFQNALGILPIASGCFLEAGDGLTFQGNHAKLFAFVAGSAGTAVSTASADKRL 120
QY 118 TFIQFSSLSFIASPGSSIT-TCKGAVSCSTGSLTKVNLSLLFSKXNFSFSDNGGAIKTIL 176
Db 121 LFNDFSRSLIISCPSELLSPTQCALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINTKNF 179
QY 177 SLTGTMTGALFSENT--SSKKGAIQTSDALITGNGEVSFSDNTSSDGAALFTBASV 234
Db 180 LLSGTSQSPASFRNQAFTKGQGVVYATGTITIENSPIGVFSQKLAKSGGALYSTDNC 239
QY 235 TISNNAKYSFIDNKVTGASSSTTGDMGGGAIQAYKTSTDTKVTLTGNOMLLFSNNTSTTA 294
Db 240 SITDNFQVIFDGNNSWEAAQA-----QCGAICCC--TTTDTKVTTLTGKKNLSFNTNTALTY 292
QY 295 GGAIYVKKLEASGLTLFSLRNSVNGGTAPK--GGAIAIBOSGELSLSADSGDIYFLGNT 352
Db 293 GGAISGLKVSISAGGPTLTFQSN-ISGSAGQGGGGAINIASAGELALSATISGDTTFNNNQ 351
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A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0308

C;Superfamily: Chlamydomphila pneumoniae polymorphic outer membrane protein G

Query Match 41.1%; Score 1964; DB 2; Length 936;
Best Local Similarity 43.4%; Pred. No. 1.4e-98;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

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QY 1 MKSFPKVFSTPAIF-PLSMIAETVLDS-ASFQGNKNGFVSRESQE-DAGTTLFLK 57
DB 1 MKSSVSWLFFSIFLFSLSIAVAEVLDSNNSYDGSNGTFTTFTTDAAGATTSL 60
QY 58 GNVLTENIPGTGTAITKCFNNTKGDLTFTGNGNSLLFQTVDAAGVAGAAVNSVVDKST 117
DB 61 SDVDFQNALGIPLASCFLIEAGDLTFQGNQHALKEAFINAGSAGTVASTSAADK 120
QY 118 TTFIGFSSLSFIASPGSSIT-TKGAVSCSTGSLSTKVNLSLFSKNPSTDNCGAITKL 176
DB 121 LFNDFSRLSIISCPBLLSPGQALK-SVGNLSLTGNSQIIFTQNFSSDNGGVINTK 179
QY 177 SLGTGTMGALPSENT--SSKGGAIQTSDALTITGNOGEVFSFNTSSDGAATFEASV 234
DB 180 LLSGTSQFASERNQAFQTKGGVVIATGTITIENSPIGVFSQMLAKSGGALYSTNC 239
QY 235 TISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTISTDTKVLTLGNOMLLFSNNTSTA 294
DB 240 SITDNFQVIFDGNSAWEAQA-----QGAIC--TTTKVTLTGKNLSFTNTALTY 292
QY 295 OGAIYVKKLELASGLTILFSRNSVNGTAPK--GGAIIEBSGELSLSDSGDIVFLGNT 352
DB 293 GGAISGLKVSISAGGTLFQSN--ISSSAGQGGGAINIASAGELALSATSGDITFN 351
QY 353 VTSITPGNRSIDLTGAKMTALRSAGRAIYFYDPTITGSGTIVTVLKNVETPADSA 412
DB 352 VTNGSTST-RNAINIIDTAKVTSIAATGQSIFYDPTINPGTAASTDTLNLNADANSE 410
QY 413 LQYTGNIIFTGKLESEAAASKNLTSLKLPQVTLSSGGLSLKHGVTLSLQTOAFTQADSR 472
DB 411 IEYGGAIYVSGEKLSPTEKAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQPSGR 470
QY 473 LEMDVGTTLPEADTS-TINNLVINSSIDGAKAKIETKATSKNLTLSGTTILLDPTGTF 531
DB 471 ILMDDGTTLSAKEANLSGLAVNLSLDGTNKAAKTEAADKNTLSGTTIALIDTEGSF 530
QY 532 YENHSIRNPQSDILELK---ASGVTSTAVTPDPIMGCKRHYGYQGTWGPVWG TGAST 588
DB 531 YENHLKASATYPLELTTAGANGTITLGAULTLQBPETHYGGNW-QLSWANATSS 589
QY 589 -TATFNWTKGTGYPNPERIGSLVPSNLNNAFIDISLHYLMETANEGLQDRAFWCAGLS 647
DB 590 KIGSINWRTGTGYPSPERKSNPLNSLWGNFIDIRSNLIETKSSGEPFERELWLSGIA 649
QY 648 NFFHKDSTKTRGRFHLGGYVIGNHLTCSKILSAAPCOLFGDRDYPVAKNGQTVYG 707
DB 650 NFFYSDSMPTRGRFHLGGYALGTATTAPAEQDLTFAPCOLFGDRNRHITGNHGDYTG 709
QY 708 GLTYQHNETYISLPCKL-----RPSLSYVTEPIPVLFSGNLSYTHDNDLKTKYTTY 761
DB 710 ASLYPHHTGLEGLDIANFLWGKATRAPVWLSISQIILPSFDAKFSVLHDDNEMKYTYDN 769
QY 762 PTVKSGWGNDSFALFGGRAPICLDESALFEQYMPMKLQFYVAHQEGKQTEAREFG 821
DB 770 SIIKGSWRNDAFCADLGSPLPVISVPYLKEVEPVKVQYIYAHQQDFERYAEGRAF 829
QY 822 SSRNLNIALPIGRFPEKSCQDATNLTLGYTVDLVRNPDCQTTTLRISGDSWKTFFGN 881
DB 830 KSELINVEPIGVTFERDSKSEKGTVDLTLMLILDAYRNPCKQTSLIASDANWMAIGTN 889
QY 882 LARQALVLRAGNHFCFNSNFEAFSPFSFELRSGSRNRYNVDLGAQYQF 928
DB 890 LARQGSVRAANHFOVNPHEIFGQPAFEVRSSRNYNINLSKFCF 936
```

RESULT 9

D86546

polymorphic outer membrane protein G family [imported] - Chlamydomphila pneumoniae (strain

C;Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001

C;Accession: D86546

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: D86546

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-930 <STO>

A;Cross-references: GB:BA000008; NID:G8978818; PIDN:BAA98654.1; GSPDB:GN00142

A;Experimental source: strain J138

C;Genetics:

A;Gene: pmp_8

C;Superfamily: Chlamydomphila pneumoniae polymorphic outer membrane protein G

Query Match 40.6%; Score 1940; DB 2; Length 930;
Best Local Similarity 43.7%; Pred. No. 2.8e-97;
Matches 416; Conservative 165; Mismatches 324; Indels 48; Gaps 17;

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QY 1 MKSFPKVFSTPAIFPLSM-IAT---ETVLDSASFDGNKNGFVSRESQEDAGTTLFL 56
DB 1 MKIPLHKLISSTLVTPIILLSIATYGDASLSPTDSPDGAGGSTTTPKSTADANGTNYVL 60
QY 57 KGVNLTENIPGTGTAITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGVAGAAVNSVVDKS 116
DB 61 SGNVVI-NDAGKGTAITGCCCTETTGDTFTFGKGFSEFNTVDAGSNAGAAA-STADKA 118
QY 117 TTFIGFSSLSFIASPGSSITTKGAVSCSTGSLSTKVNLSLFSKNFSTD---NGCAITA 173
DB 119 LTFTGFSNLSFIAAGTIVASGKSTLS-SAGALNLTGNTILFSQNVSEANNNGCAITA 177
QY 174 KTLSTGTMTGALPSENTSSKGGAIQTSDALTITGNOGEVFSFNTSSDGAATFEAS 233
DB 178 KTLSTSGNTSSITFTTSNAXKLGGAIYSAAASISGNTGQLVFMNKGCTGGGALGFAS 237
QY 234 VTISNNAKVSFIDNKVTGASSSTTGDMSGGAICAYKTISTDTKVLTLGNOMLLFSNNTST 293
DB 238 SSITQNSLSLFFSGNTATDAAG-----KGGAIYCEKTEGETPILTISGNKSLTFAENSVT 291
QY 294 AGGAIYVKKLELASGLTILFSRNSVNGTAPKGAIAIEDSGELSLSDSGDIVFLGNTV 353
DB 292 QGGAICAHGLDLSAAGPTILFSNNRCGNTAAGKGAIAIADSGLSLSANQGDITFLGNTL 351
QY 354 TSTT-PGNRRSIDLGTSAKMTALRSAGRAIYFYDPI---TTGSGTIVTVLKNVETPA 409
DB 352 TSTSAPTSTRNAIYLGSSAKITNLRAAQQSIFYDPIASNTTGAS---DVLTTINQPOS 407
QY 410 DSALQYTGNIIFTGKLESEAAASKNLTSLKLPQVTLSSGGLSLKHGVTLSLQTOAFTQQA 469
DB 408 NPLDYSGTIVFSGEKLSDAEKADNFTSILKQPLALASGTALAKGNVELDVNGTQTE 467
QY 470 DSRLEMDVGTTLPEADTSTIN--NLVINISSIDGAKAKIETKATSKNLTLSGTTILLDP 527
DB 468 GSTLLMQPTKLUK-ADTEAISLTSLVLDLSALEGNKSVSIETAGANKTTLTSPVFDQS 526
QY 528 TGTTFENHSIRNPQSDILELKAS-----GVTSTAVTPDPIMGCKRHYGYQGTW 578
DB 527 SGNFYESTHINAQTPQLVVFYTAATAASDIYTDALLTSPVQPEP-----HYGQGHWE 580
QY 579 PIVWGTGASTTATFNWTKGTGYPNPERIGSLVPSNLNNAFIDISLHYLMETANEGLQD 638
DB 581 ATWADTSTAKSGTMTWVTGYNPNERRASVVPDSLWSFSTDIRTLQQIMTQANSIYQ 640
QY 639 RAFWCAGLSNPFPHKOSTKTRGRFHLGGYVIGNHLTCSKILSAAPCOLFGDRDYPV 698
DB 641 RGLWASGTANFPHKOKSGTGNQAFRHKSYGYIVGGSAAEDFSENI FSVAFCOLFGDKDLFI 700
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Qy	470	DSRLMDVGTTLLEADPTSTIN--NLVINISSIDGAKAKIETKATSKNLTLSGTTLLDLP	527
Db	468	GSTLIMQPGTKLK-ADTEAISLTKLVLDLSALEGKNSVSIETAGANTITITLSPVLFQDS	526
Qy	528	TGTFEYENSLRNPQSDVILELKAS-----GTVTSTAVTPDPIMGEKPHYGYQGWTWG	578
Db	527	SGNFYESTHINQAFTQPLVVFVTAATAASDIYDALLTSPVQTPEP-----HYGYQGHWE	580
Qy	579	PIVMGTGASTTATFNWTKTYIPNPERIGSLVPSNLWNAFIDISSLHLYMETANEGLQD	638
Db	581	ATWADTSTAKSGTMTVWTGYNPNPERRASVVPDLSWASFTDRTLQOIMTSQANSIYQQ	640
Qy	639	RAFCWAGLSNPHKDKSTKTRGFRHLHSGGVITCGNLHTCSDKILSAAFCQLGFRDRDYPV	698
Db	641	RGLMASGTANFPHKDKSGTGNQAFRHKSXYGIYVGGSAEDFSENIFSVAFCQLGFKDKDLFI	700
Qy	699	AKNQGTVVGGTLYLYOHNETYISLPCKLRPC--SLSVYVPTPIVLFGSNLSYTHTDNDLKT	756
Db	701	VENTSHNYLASLYLQHRAFLGLP---MFSFGSITDMLKDIPILINLQLSYSYTKNDMDT	757
Qy	757	KYTTYPTVKGSGNDSFALEFGGRAPICL-DESALFEQYMPFMKLQFYVYAHQEGFKEQGT	815
Db	758	RYTSYPEAQQSGWTNNSGALELGSLALYLPKEAPFFQGYFPFLKFQAVYSRQQNFKEGSA	817
Qy	816	EAREPGSSRLYNALPIGIRFPKESDCQATYNLTGYTVDLVRSNPDCDCTTLTRISGDSW	875
Db	818	EARAFDDGDLVNCSPVIGIRLEKISDEKKNFBI SLAYIGDVYRKNPRSRITSLMVSGASW	877
Qy	876	KTFGTLNARQALVLRAGNHCFNSNPEAFSQFSFELRGSSRNYNVDLGAKYOF	928
Db	878	TSLCKNLARQAFLAGSGSHLITSPVELSGEAAEYELRGSASHIYNVDCGLRVSF	930

RESULT 11

D72078

polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CWL029)

C/Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001

C/Accession: D72078

R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999

A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A/Reference number: A72000; MUID:99206606; PMID:10192388

A/Accession: D72078

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-930 <ARN>

A/Cross-references: GB:AB001627; GB:AE001363; NID:g4376721; PIDN:AAD18590.1; PID:g4376722

A/Experimental source: strain CWL029

C/Genetics:

A/Gene: pmp_8

C/Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Query Match	40.6%;	Score 1936;	DB 2;	Length 930;
Best Local Similarity	43.5%;	Pred. No. 4.7e-97;		
Matches	415;	Conservative 165;	Mismatches 325;	Indels 48; Gaps 17;

Qy 1 MKSFPKPVSTFAIPLSM-IAT---ETVLDSASAFDGNKGNFVSRESQEDAGTTLF 56

Db 1 MKIPLKLLISLTVPIILLSIATYQADASLSPTDSFDGAGGSTFTPKSTADANGTNYVL 60

Qy 57 KGNVTLENIPTGTHAIKSCFNNTKGLTFTGNGNSLLTQTVDAGTVAGAAVNSVVDKS 116

Db 61 SGNVYI-NDACGKTALTGCCFTFTTGDLTFTTKGYSFSFNTVDAGSNAGAAA-STTADKA 118

Qy 117 TTFIGFSSLFIASPGSSITTKGAVSCSTGSLSTKNVSLLSFKNFSTD--NGGALTA 173

Db 119 LTFGFSNLFIAPDGTIVAGSKSTLS-SAGALNTDNGTILFISQVNSFNANNNGAITT 177

Qy 174 KTLSTGTMTSALPSENTSSKKGGAQTSDALTTTNGQGEVFSFSDNTSSDGAALFTFAS 233

Db 178 KTLISGNTVSTITFTNSAKKLGGAIYSSAAASISGNTGOLVPMNKNKGTGGCAIGFEAS 217

Qy 821 GSSRLVNLALPIGIRFDKESDCQDA-TYNLTGLGYTVDLVRSPNCDCTTTTLRISGDSWKTFG 879
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 821 SIGRLNLSIPVGAKF-VQGDIGDSTYTDLSGFFSDVVRRNPQTATLVMSPDSDKIRG 879
 Qy 880 TNLARQALIVPAGHFCNSNFAPSQFSFELRGSSRNYYNDVLGAKYQF 928
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 880 GNLSRQAFLLRGSNNYYNSCNELFGHYAMELRGGSSRNYYNDVGTKLRF 928

RESULT 14
 F81591

Polymorphic membrane protein G family CP0302 [imported] - Chlamydophila pneumoniae (strain C) Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
 C:Accession: F81591
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, P.A.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: AB1500; MUID:20150255; PMID:10684935
 A:Accession: F81591
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-949 <REA>
 A:CROSS-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38159.1; PID:g7189225
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CP0302
 C:Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Query Match	38.9%	Score 1855;	DB 2;	Length 949;
Best Local Similarity	42.7%	Pred. No. 1.2e-92;		
Matches	405;	Conservative 171;	Mismatches 331;	Indels 42;
Gaps	20;			

Qy 1 MKSFPKFVSTFAIPP--LSMIATETVLDSSAFDGN-KNGNPSVRSEODAGTTYLPK 57
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 22 MKTSIPWLVSVSLAFLSCHLOSLANEELLSPDDSFNGNIDSGTFTPKTS---ATTYSLT 77

Qy 58 GNTVLENI PGTGAI TKSCFNNTKGDLTETGNGSNLAFQTVDAGTVGAANSSVVDKST 117
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 78 GDVFYE-PKGTPLSOSCFQTTDNLTFLNGHSLTFGFIDAGTHAGAA-STTANKNL 135

Qy 118 TFIGFSSLFIASPGSSITTKGAVSCSTGSLSTKNVLSLFSKNFSTDNGGAI TAKTLS 177
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 136 TFSGFSLLSPDSSPTVTTCQGTL-SAGGVNLENIRKVAVAGNSTADGAI KGASF 194

Qy 178 LTGHTMSALPSENVSXKKGAI QTSDALTTGNGEVSFSDNTSSDGAAIPEASVTIS 237
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 195 LTGTSGDALFNSNSSSTKGGAIAITAGARIANNITYRVFLSNIASTSGAIDDEGTSILS 254

Qy 238 NNAKVSFIDNKVTGASSTTGDMSGGAICAKTSDTKVTLTGNOMLLFSNNSTTAGCA 297
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 255 NNKELYF-----EGNAAKTI----GGAI CNTKASGPPELL ISNNKTLPASNVARTSGGA 305

Qy 298 IYVKKL ELAGGLTFLSRNSYNGTAPKPGAIAIEDSGELSADS GDIVFLGNTWTST- 356
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 306 IHAKUALSSGGFTFEFLRNVS SAT-PKGGAISIDASGELS SAETGNITFVRNLTITTG 364

Qy 357 -TPGTNRSSIDLGTSAKWTAIRLSAAGR AIYPDPIT TGSGSTTVTDVLKVNTEPADSALQY 415
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 365 STDTPKENAINISNGXFTFLRAAKNHTIFPYDPIT--SEGTS DVLKINNGSAGALNPY 422

Qy 416 TGMII FTGK LSETAADSKNLTS KLIQPVTLSGCTL SLKHGVTL QTCAFTQQADSRLEM 475
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 423 QGITLFSGETLTAD ELKVAO NLKSSFTQPVLSLGGKULLQKGVLTLESFSQEAGSLGM 482

Qy 476 DVGFTTLE-PADTST INNLVINISIDCAKAKIETKATSKNLTL SGTTILLDPTGFYEN 534
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 483 DSGTTLSTTAGS ITINLGIN VDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYES 542

Qy 535 HS LRNPQSVDILELKASGTVTS-----TAVTPDPIMGEKFHYGYO GTMGPIVMGTGA STT- 589
 Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
 543 HMFSDHQLFLLKITTVDADVTNVDISLIPVPAEDPNSEYGFQGOANN-VNWTIDTA NT 601

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:14:22 ; Search time 50 Seconds
(without alignments)
5821.955 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFPKVFSTFAIFPLSM.....FELGGSSRNVDLGAQYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4774	100.0	928	10	US-09-428-122-2
2	3865	81.0	746	15	US-10-312-273-19
3	2802.5	58.7	597	15	US-10-289-762-29
4	2048	42.9	928	15	US-10-312-273-95
5	1982	41.5	928	15	US-10-312-273-33
6	1965	41.2	936	9	US-09-452-380-3
7	1965	41.2	936	12	US-10-282-122A-54679
8	1965	41.2	936	14	US-10-324-129-3
9	1965	41.2	936	15	US-10-312-273-153
10	1946.5	40.8	925	9	US-09-452-380-4
11	1946.5	40.8	925	14	US-10-324-129-4
12	1940	40.6	930	15	US-10-289-762-470
13	1936	40.6	930	12	US-10-282-122A-54680
14	1936	40.6	930	15	US-10-312-273-45
15	1917.5	40.2	927	15	US-10-289-762-472

16	1915	40.1	926	10	US-09-738-269-57	Sequence 57, Appl
17	1915	40.1	926	13	US-10-023-437-57	Sequence 57, Appl
18	1856	38.9	949	15	US-10-289-762-478	Sequence 478, Appl
19	1855	38.9	928	12	US-10-282-122A-54681	Sequence 54681, A
20	1855	38.9	928	15	US-10-312-273-115	Sequence 115, Appl
21	1656.5	34.7	839	10	US-09-738-269-23	Sequence 23, Appl
22	1656.5	34.7	839	13	US-10-023-437-23	Sequence 23, Appl
23	1573	32.9	841	12	US-10-282-122A-54677	Sequence 54677, A
24	1573	32.9	841	15	US-10-312-273-139	Sequence 139, Appl
25	1572.5	32.9	942	15	US-10-289-762-474	Sequence 474, Appl
26	1442.5	30.2	922	15	US-10-312-273-41	Sequence 41, Appl
27	1437.5	30.1	922	9	US-09-886-468-19	Sequence 19, Appl
28	1437.5	30.1	922	12	US-09-889-468-19	Sequence 19, Appl
29	1417.5	29.7	922	15	US-10-289-762-15	Sequence 15, Appl
30	1383.5	29.0	1407	12	US-10-282-122A-54678	Sequence 54678, A
31	1383.5	29.0	1407	15	US-10-312-273-31	Sequence 31, Appl
32	1377.5	28.9	973	15	US-10-312-273-3	Sequence 3, Appl
33	1377.5	28.9	973	16	US-10-352-618-2	Sequence 2, Appl
34	1259	26.4	671	15	US-10-289-762-468	Sequence 468, Appl
35	1214	25.4	230	15	US-10-289-762-30	Sequence 30, Appl
36	1203.5	25.2	507	15	US-10-289-762-32	Sequence 32, Appl
37	1150	23.7	1132	15	US-10-289-762-466	Sequence 466, Appl
38	1128	23.6	1012	12	US-10-701-844-2	Sequence 2, Appl
39	1128	23.6	1012	16	US-10-766-711-2	Sequence 2, Appl
40	1126.5	23.6	1006	9	US-09-841-132-190	Sequence 190, Appl
41	1124.5	23.6	982	9	US-09-841-132-176	Sequence 176, Appl
42	1120.5	23.5	1013	16	US-10-467-534-9	Sequence 9, Appl
43	1117.5	23.4	984	12	US-10-701-844-43	Sequence 43, Appl
44	1117.5	23.4	984	16	US-10-766-711-43	Sequence 43, Appl
45	1110.5	23.3	1013	12	US-10-701-844-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

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US-09-428-122-2
; Sequence 2, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE OF INVENTION: US95 THERIOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-09-428-122-2
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Query Match	100.0%	Score 4774;	DB 10;	Length 928;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 928;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKSFPKVFSTFAIFPLSMIATEVLDSSASFDGKNGNFVRSQEDAGTYLFGNV	60	
Db	1	MKSFPKVFSTFAIFPLSMIATEVLDSSASFDGKNGNFVRSQEDAGTYLFGNV	60	
Qy	61	TLENTPGTGTATKSCFNNTKGLFTGTGNSLLFQTVTDAGTVAGAAVNSSVVDKSTTFI	120	
Db	61	TLENTPGTGTATKSCFNNTKGLFTGTGNSLLFQTVTDAGTVAGAAVNSSVVDKSTTFI	120	
Qy	121	GFSSLSFIASPGSSITTKGAVSCSTGSLILTKNLSLLFSKNFSTDNGGAIKATKLSLTG	180	

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Db 121 GFSSLSFIASPGSITTTKGAVSCSTGSLSKTNVSLFLFSKNFSTNDGGAITAKTLSTG 180
Qy 181 TTMGALFSENTSSKGGAIQTSALTTIGNQGEVSFSDNTSSDGAALFTEASVTISNNA 240
Db 181 TTMGALFSENTSSKGGAIQTSALTTIGNQGEVSFSDNTSSDGAALFTEASVTISNNA 240
Qy 241 KVSFIDNKVTGASSSTTGDMSGGAI CAYKTS TDTKVTLTGNQMLLFSNNTSTTAGGAIYV 300
Db 241 KVSFIDNKVTGASSSTTGDMSGGAI CAYKTS TDTKVTLTGNQMLLFSNNTSTTAGGAIYV 300
Qy 301 KKLDELASGLTLFPRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNTVTSITPGT 360
Db 301 KKLDELASGLTLFPRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNTVTSITPGT 360
Qy 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSITVTVDLVKNETPADSALQVTGNI 420
Db 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSITVTVDLVKNETPADSALQVTGNI 420
Qy 421 FTGEKLSATEAADSKNLTKLPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 480
Db 421 FTGEKLSATEAADSKNLTKLPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 480
Qy 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTFFYENHSLRNP 540
Db 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTFFYENHSLRNP 540
Qy 541 QSYDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 600
Db 541 QSYDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 600
Qy 601 PNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 660
Db 601 PNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 660
Qy 661 FPHLSGGVYVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYIS 720
Db 661 FPHLSGGVYVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYIS 720
Qy 721 LPCKLRPCSLSVPTPEI PVLFSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGR 780
Db 721 LPCKLRPCSLSVPTPEI PVLFSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGR 780
Qy 781 APICLDESALFEQYMPFMKLPQVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKES 840
Db 781 APICLDESALFEQYMPFMKLPQVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKES 840
Qy 841 DCQDATYNLTGYTVDLVRSPNDC TTTLRISGDSWKFTGTLARQALVLRAGNHFCFNSN 900
Db 841 DCQDATYNLTGYTVDLVRSPNDC TTTLRISGDSWKFTGTLARQALVLRAGNHFCFNSN 900
Qy 901 FFAFSQFSFELGSSRNYNVDLGAKYQF 928
Db 901 FFAFSQFSFELGSSRNYNVDLGAKYQF 928

RESULT 2
US-10-312-273-19
; Sequence 19, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
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; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqMin99, version 1.02
; SEQ ID NO 19
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-19

Query Match      81.0%; Score 3865; DB 15; Length 746;
Best Local Similarity 100.0%; Pred. No. 6,1e-281;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 MSALFSENTSSKGGAIQTSALTTIGNQGEVSFSDNTSSDGAALFTEASVTISNNAKV 242
Db 1 MSALFSENTSSKGGAIQTSALTTIGNQGEVSFSDNTSSDGAALFTEASVTISNNAKV 60
Qy 243 SFIDNKVTGASSSTTGDMSGGAI CAYKTS TDTKVTLTGNQMLLFSNNTSTTAGGAIYVK 302
Db 61 SFIDNKVTGASSSTTGDMSGGAI CAYKTS TDTKVTLTGNQMLLFSNNTSTTAGGAIYVK 120
Qy 303 LELASGGLTLFPRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNTVTSITPGTNR 362
Db 121 LELASGGLTLFPRNSVNGGTAPKGGAI AIEDSGELSLSDSGDIVFLGNTVTSITPGTNR 180
Qy 363 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSITVTVDLVKNETPADSALQVTGNIPT 422
Db 181 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSSITVTVDLVKNETPADSALQVTGNIPT 240
Qy 423 GEKLSATEAADSKNLTKLPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 482
Db 241 GEKLSATEAADSKNLTKLPVTLSSGGLSLKHGVTLOQAFQOADSRLMDVGT 300
Qy 483 PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTFFYENHSLRNP 542
Db 301 PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTFFYENHSLRNP 360
Qy 543 YDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 602
Db 361 YDILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVIMVGTGASTTATFNWTKGYI 420
Qy 603 PERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 662
Db 421 PERIGSLVPSNLWNAFIDISSLHYLMETANEGLQGDRAFWCAGLSNFFHKDSTKTRRG 480
Qy 663 HLSGGVYVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYISLP 722
Db 481 HLSGGVYVGNLHTCSDKILSAAPCOLFGRDRDYFVAKNQGTYYGGLTYQHNETYISLP 540
Qy 723 CKLRPCSLSVPTPEI PVLFSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGRAP 782
Db 541 CKLRPCSLSVPTPEI PVLFSGNLSYTHTDNDLTKYTTPTVKGSGNDSFALEFGGRAP 600
Qy 783 ICLDESALFEQYMPFMKLPQVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKESDC 842
Db 601 ICLDESALFEQYMPFMKLPQVYAHQGEKFEQGTAREFGSSRLVNLALPIGIRFDKESDC 660
Qy 843 QDATYNLTGYTVDLVRSPNDC TTTLRISGDSWKFTGTLARQALVLRAGNHFCFNSNPF 902
Db 661 QDATYNLTGYTVDLVRSPNDC TTTLRISGDSWKFTGTLARQALVLRAGNHFCFNSNPF 720
Qy 903 FFAFSQFSFELGSSRNYNVDLGAKYQF 928
Db 721 FFAFSQFSFELGSSRNYNVDLGAKYQF 746
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```
RESULT 3
US-10-289-762-29
; Sequence 29, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 29
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-29

Query Match      58.7%; Score 2802.5; DB 15; Length 597;
Best Local Similarity 93.8%; Pred. No. 2.2e-201;
Matches 560; Conservative 5; Mismatches 21; Indels 11; Gaps 3;

QY 149 LSLTKVLSLFSKNSFTDNGGAIATAKTLSTLTGTMGALFSENSSKKGGAIQTSALTIIT 208
Db 1 LKFDKNVLSLFSKNSFTDNGGAIATAKTLSTLTGTMGALFSENSSKKGGAIQTSALTIIT 60
QY 209 GNOGEVSFSDNTSSDGAALFTEASVTISNNKVSFIDNKKVTCASSSTTGDMGGGAICAY 268
Db 61 GNOGEVSFSDNTSSDGAALFTEASVTISNNKVSFIDNKKVTCASSSTTGDMGGGAICAY 120
QY 269 KTSITDKVTLTGQMLLFNSNTSTTAGGALYVKKLELASGGLTLFRNSVNGGTAPKGA 328
Db 121 KTSITDKVTLTGQMLLFNSNTSTTAGGALYVKKLELASGGLTLFRNSVNGGTAPKGA 180
QY 329 IAEDESGELSLGADSDIIVFLGNVTSTTPTNRSSIDLTSAMTALRSAGRAIYFYD 388
Db 181 IAEDESGELSLGADSDIIVFLGNVTSTTPTNRSSIDLTSAMTALRSAGRAIYFYD 240
QY 389 PIITGSSSTTVDLKYNETPADSALQYGNLFTGKLSSETAADSKNLTSKLLQPVTL 448
Db 241 PIITGSSSTTVDLKYNETPADSALQYGNLFTGKLSSETAADSKNLTSKLLQPVTL 300
QY 449 GGTLSLKHGVTLLQTAFTQOADSRLMDVGTTLLEPADTSTINNLVINISIDCAKKAKIE 508
Db 301 GGTLSLKHGVTLLQTAFTQOADSRLMDVGTTLLEPADTSTINNLVINISIDCAKKAKIE 360
QY 509 TKATSKNLTLSGTITLLDPTGTFYENHSLRNPOSYDILELKASGTVTSTAVTDPDPMGEK 568
Db 361 TKATSKNLTLSGTITLLDPTGTFYENHSLRNPOSYDILELKASGTVTSTAVTDPDPMGEK 420
QY 569 FHYGYGTWGPVWGTGASTTATFNKTKGYPNPERIGSLVPSNLWNAFIDISSLHYLM 628
Db 421 FHYGYGTWGPVWGTGASTTATFNKTKGYPNPERIGSLVPSNLWNAFIDISSLHYLM 480
QY 629 ETANEGLOQDRAFCWAGLSNFFHKDSTKTRRGRHLSGGYVIGNLHTCSDKILSAFQC 688
Db 481 ETANEGLOQDRAFCWAGLSNFFHKDSTKTRRGRHLSGGYVIGNLHTCSDKILSAFQC 540
QY 689 LFGRRDRDYFVAKNQG-TVVGGTLYYOHNETYIS-----LPCKLR-PCSLSYVP 734
Db 541 LFGRRDRDYFVAKNQYSLRNSRLPAQRNLYLSLQTTALFVVLCSYRDSCLFRKP 597

RESULT 4
US-10-312-273-95
; Sequence 95, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
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; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 95
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-95

Query Match      42.9%; Score 2048; DB 15; Length 928;
Best Local Similarity 46.5%; Pred. No. 1.7e-144;
Matches 442; Conservative 144; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSPFPKYPF-STFAIF---PLSMIATETVLDSSAFDGNKN-GNFSVRESQEDAGTTYL 55
Db 1 MKSQFSLVLSFTLACFTSCSTVFAAENIGPSDSFDGSGTNGTTPKNT--TTGIDYT 58
QY 56 FKQNVLTENIPGTGTRAITKSCFNNTKGDLTFTGNGNSLLPOTVDAGTVAGAANNSSVDK 115
Db 59 LTGDTITLQNL-GDAAALTKGCFSDTTESLSFAGKGYSLFLNIKS-SABGAAL-SVYTDK 115
QY 116 STTFIGFSSLSFTASPGSSITT--GKGVSCSTGSLTKNVSLLFSKNFSTDNGGAI 173
Db 116 NLSLTFGSSLTFLAAPSIVITTPSGKGVKCG-GDLTFDNNGTILFKQCYEENGAI 174
QY 174 KTLSTGTMTSALFSENSS---KKGGAIQTSALTIITGNOGEVSFSDNTSSDGAALFT 230
Db 175 KNLKLNKSGSISFEGNKSSATGKKGALCATGTVDTTNTAPTFLSNIAEAGGAINS 234
QY 231 EASVTISNNKVSFIDNKKVTCASSSTTGDMGGGAICAYKTSTDTKVTLTGNOMLLFNSNT 290
Db 235 TGNCTITGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNQSVTFSGNQ 283
QY 291 STTAGGAIYVKKLELAS--GGLTLFRNSVNGGTAPKGAIAIEDSGELSLGADSDIIVF 348
Db 284 AVANGGAIYAKKLTLASGGGVSPFTIIVQGTAGNGGAI SILAAGETCSLAEAGDIITF 343
QY 349 LGNTVTSTTP-GTNRSSIDLTSAMTALRSAGRAIYFYDPIITGSSSTTVTDVLKVN 407
Db 344 NGNAIVATTPTQTKRNSIDIGSTAKITNLRAISGHSIFFYDPIITANTAASTDNLNKA 403
QY 408 PADSALOYTGNIIFTEGKLSSETAADSKNLTSKLLQPVTLSSGTLSLKHGVTLLQTAFTQ 467
Db 404 DAGNSTDYSGSIVFSGEKLSEDEAKVADNLTLKQPVTLTAGNLVLRKGVTLDTKGFTQ 463
QY 468 QADSRLMDVGTTLLEPA-DTSTINNLVINISIDGAKKAKIETKATSKNLTLSGTITLLD 526
Db 464 TAGSSVIMDAGTTLKASTEETVTLGLSIPVDSLGSGKKVVI AASAKRNVALSGPILLD 523
QY 527 PTGTFYENHSLRNPOSYDILELKASGTVTSTAVTDPDPMGEKHYGYGTWGPVW---- 582
Db 524 NQGNAYENHDLCKTQDFSFVQLSALGTATTDVPAVPTVATPTHYGYGTW-GMWVDT 582
QY 583 -GTGASTTATFNKTKGYPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLOQDRAFC 641
Db 583 ASTPKTKATLATWNTGVLNPERQGPLVPSNLWGSFSDIQAIOGVIERSAULTLCSDRGF 642
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```
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-452-380-3

Query Match      41.2%; Score 1965; DB 9; Length 936;
Best Local Similarity 43.4%; Pred. No. 2.9e-138;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSSFFKVFSTFAIF-PLSMIAETEVLDS-ASFQGNKNGFVSRESOE-DAGTTLFLK 57
Db 1 MKSSVWLFSSIPLESLSIVAEEVTLDSNNSYDGSNGTTFVSTDDAAAGTTYSLL 60
QY 58 GNVTLNIPGTGTAITKSCFNNTKGLDFTFGNGSNLLFQTVDAGTVAGAAVNSVVDKST 117
Db 61 SDVSVFNAGALGPIPLASGCGFLEAGGDLTFQGNHAKLFAFINAGSSAGTVASTSAADKNL 120
QY 118 TFGFSSLSFIASPGSSIT-TGKGVSCSTGSLTKNVLSLLFSKMFSDNGGAIKTATL 176
Db 121 LFNDFSLRSLIISCPSSLSPGQCALK-SVGNLSLTGNSQIIIFQNFSSDNGGVINTKNF 179
QY 177 SLTGTTMSALFSENT--SSKKGCAIQTSDALTITGQGVSVFSDNTSSDGAIFTEASV 234
Db 180 LLSGTSQFASFRNQAFQTKQGGVVATGTIIENSFGIVSFQNLAKSGGALYSTDNC 239
QY 235 TISNNAKVSFIDNKVTGASSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFNNSTTTA 294
Db 240 SITDNFQVIFDGNSAWEAAQA-----QGGAICC--TTTDKVTLTGNKLSFTNNALT 292
QY 295 GGAIVYKKELEASGGTILFSRNVNGGTAPK--GGAIAEDSGELSLSDSGDIVFLGNT 352
Db 293 GGAISGLKVSISAGGPTLFQSN-ISGSSAGCGGGAINIASAGELALSATSGDITENNQ 351
QY 353 VSTTTEGTRNSDILGTSAKWTALRAAGRAIYFDPITGTSSTTVTVLKVNETPADSA 412
Db 352 VINGSTST-RNAIITDITAKVTISRAATGQSIYFDPITNPGTAASDTLNLMLADANSE 410
QY 413 LQYTGNIITFGEKLSETEADSKNLAKLPVTLGGTILSLKHGVTLOTQAFQOADS 472
Db 411 IEYGAIVFSGEKLSPTEKAIANVTSTIRQPAVLARGDLVLRDGVTVTFKDLTQSPGR 470
QY 473 LEMDVGTTLEPADTS--TINNLVINISIDGAKAKIETKATSKNLTLSGTITLLDPTGF 531
Db 471 ILMDCGTTLSAKENIISLGLAVNLSSDGTNKAALKTEAADNLSLGTIALIDTEGSP 530
QY 532 YENHSLRNQSDILELK--ASGTVTSTAVTPDPIMGEKFHYGQGTWGPVWGTGAST 588
Db 531 YENHNLKSASTYPLELTTAGAGTITLGAISLTTLQEPETHYGYQGNW-QLSWANATSS 589
QY 589 -TATFNWTKTYIPNERIGSLVPSLNWAFIDISLHYLMETANEGLOGDRAPWCAGLS 647
Db 590 KIGSINWTRTYGIPSPERKSNLPLNSLWGNFDIRSINQLIETKSSGEPFERELWLSGIA 649
QY 648 NFPHKDSITRGRFRLHSGYVIGNHLHSCDKLSAFCQLPGRDRDVFVAKNQGTVVG 707
Db 650 NPFYRDSMPTRHGRHISGAYALGITATTAPEDQLTFAFCQLFARDNRHITGNHGDYTG 709
QY 708 GTLYXOHNETYISLPCKL-----RPCSISYVTEIPVLPFSGNLSYTHTDNDLTKYTY 761
Db 710 ASLYFHHTTEGLFDIANFLMGKATRAFWLSEISQIILPSFDAKFSYLHTDNNHMTYTDN 769
QY 762 PTWKGWGNDSFALEGGRAPICLDESALFEQYMPFMKLQFVYAHQGEKFEQTEAREFG 821
Db 770 SLIKGSWRNDAFCADLGASLPFVISPYLLKVEPEPVKVQYIYAHQDDFERHAEGRAF 829
QY 822 SBLVNLALPIGRFPKESDQDATNLTGLYTVDLVRNPDCTTLRLSGDSWKTFTGN 881
Db 830 KSELINVEIPIGVTFERDSKSEGTVDLTIMYILDAYRRNPKQCTSLIASDANWMAYG 889
QY 882 LARQALVLAGNHFNCNSNFEAFSOFSELRGSSRNVDLGAKYOF 928
Db 890 LARQGSFVRAANHFQVNPHEIFGQFAFEVRSRRNTNLTGSKFCF 936
```

```
RESULT 7
US-10-282-122A-54679
; Sequence 54679, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54679
; LENGTH: 936
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54679

Query Match      41.2%; Score 1965; DB 12; Length 936;
Best Local Similarity 43.4%; Pred. No. 2.9e-138;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSSFFKVFSTFAIF-PLSMIAETEVLDS-ASFQGNKNGFVSRESOE-DAGTTLFLK 57
Db 1 MKSSVWLFSSIPLESLSIVAEEVTLDSNNSYDGSNGTTFVSTDDAAAGTTYSLL 60
QY 58 GNVTLNIPGTGTAITKSCFNNTKGLDFTFGNGSNLLFQTVDAGTVAGAAVNSVVDKST 117
Db 61 SDVSVFNAGALGPIPLASGCGFLEAGGDLTFQGNHAKLFAFINAGSSAGTVASTSAADKNL 120
QY 118 TFGFSSLSFIASPGSSIT-TGKGVSCSTGSLTKNVLSLLFSKMFSDNGGAIKTATL 176
Db 121 LFNDFSLRSLIISCPSSLSPGQCALK-SVGNLSLTGNSQIIIFQNFSSDNGGVINTKNF 179
QY 177 SLTGTTMSALFSENT--SSKKGCAIQTSDALTITGQGVSVFSDNTSSDGAIFTEASV 234
Db 180 LLSGTSQFASFRNQAFQTKQGGVVATGTIIENSFGIVSFQNLAKSGGALYSTDNC 239
QY 235 TISNNAKVSFIDNKVTGASSTTGDMSGGAICAYKTSTDTKVTLTGNQMLLFNNSTTTA 294
Db 240 SITDNFQVIFDGNSAWEAAQA-----QGGAICC--TTTDKVTLTGNKLSFTNNALT 292
```

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QY 295 GGAIYVKKLELASGLTLFSRNSVNGTAPK--GGAIATEDSGELISADSGDIVFLGNT 352
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 293 GGAIISGLKVSISAGPPTLFQSN-1SGSAGOGGGGAINIASAGELALSATSGLDITFNNQ 351
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 353 VTSTTPGNNRSSIDLGTSAKMTALRSAGRAIYFYDPTTSGSTVTVDLVKVNTPADSA 412
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 352 VTNGSTST-RNAINIIDTAKVTSIRATGQSIYFYDPTTNPCTAASDTTLNLNADANSE 410
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 413 LQYTGNIIFTGKLESEADSKNLTSLKLOPVTLSGGTSLSKHGVTLTQTAFTQADSR 472
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 411 IEYGAIIVFSGEKLSPTEKALAAVNTSIROPVAVLARGDLVLRDGVTVTFKDLTQSPGR 470
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 473 LEMDVGTTLEPADTS-TNNIVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTF 531
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 471 ILMDDGTTLSAKEANLSGLAVNLSSLDGNTKAALKTEAADKNLSLSTIALIDTEGSF 530
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 532 YENHSLRNPOQSDILELK---ASGTVTSTAVTPDPIMGEKHYGQGTGWGPIVWGTGAST 588
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 531 YENHNLKSASTYPLLELTTAGANGTITLGAALSTLTLPBETHYGYQGNW-QLSWANATSS 589
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 589 -TATFNWTKTGIVNPERIGSLVPSNLSMNAFIDISSLHVMETANEGLQGDRAFWCAGLS 647
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 590 KIGSINWRTGTVIPSERKSNLPLNSLWGNFIDIRSIQLIETKSSGEPFERELWLSGIA 649
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 648 NFFHKDSTKTRRGFRHLGGVIGVGNLHTCDKILSAAFCOLFGRDRDRYFVAKNQGTVYG 707
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 650 NFFYRDSMPTRHGFRHISGGYALGITATTPAEDQLTFAFCQLFARDNRHITGKNHGDYV 709
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 708 GTLYVQHNETYISLPCKL-----RPSLSVYVPTPIVLFSGNLSTYTHDNDLTKYTTY 761
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 710 ASLYPHHTEGLEGLFDIANFLWGKATRAPWVLSLSQIIPLSFADKFSYLHTDNHMKTYTND 769
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 762 PTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLQFYAHQEGFKEQGTAREFG 821
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 770 SIIKGSWRNDAFCADLGASLPVIVSVPYLLKEVEFPVKVQYIYAHQQDFYERHAEGRAPN 829
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 822 SSSLNVALPIGIREDKESDCODATYNLTGYTDLVRSNPDCTTLTIRSGDSMKTFTGN 881
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 830 KSELINVEIPIGTVTERDSKSEKGYDITLMYILDAYRNPCKQTSLIASDANWYAGTN 889
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 882 LARQALVLRAGNHFCNFSNFEAFSOFPELGRSSRNYNVDLGAKYQF 928
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 890 LARQGFVSRAANHFOVNPHMEIFGQFAFEVRSRNRNNTNLGSKFCF 936
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 8
US-10-324-129-3
; Sequence 3, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN ET AL.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
; FILE REFERENCE: 7813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 936
; TYPE: PRN
; ORGANISM: Chlamydia pneumoniae
US-10-324-129-3

Query Match 41.2%; Score 1965; DB 14; Length 936;
Best Local Similarity 43.4%; Pred. No. 2.9e-138;
Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSSPKFFVFSFAIF-PLSMIATEIVLDSS-ASFDGNKNGNFSVRESQE-DAGTTLFK 57
```

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Db 1 MKSSVMSLFFSSIFLPSLSIVAABEVTLDDSNNSYDGSNGTTFVFSFTDAAAGTYSLL 60
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 58 GNVTELENIPTGTATITKSCFNNTKGDLTFTGNGNSLLFQTVDAAGTVAGAAVSSVVDKST 117
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 61 SDVSFQVAGALGIPLAGSCFLEAGDILTFQGNQHALKEAFINAGSSAGTVASTSAADKNL 120
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 118 TFIQFSSLSFIASPGSSIT-TGKAVSGSTGSLTKXVLSLLFKNFSTNDGGALITAKTL 176
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 121 LFNDFSRLLSIISCFSLSPGQCALK-SVGNLSLTGNSQIIFTONFSSDNGGVINTKNF 179
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 177 SLTGTTMSALPSENT--SSKKGAIQISDALTITGNOGEVFSFSDNTSDSGAALFTASV 234
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 180 LLSGTSPAFSFRNOAFTGQGGVYVATGTTIENSPIGVFSQNLAKSGGALSTUNC 239
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 235 TISNNAKVSFIDNKNVTGASSSTTGDMSGCAICAYKTSTDTTTLTGNOMLLFSNNSTTA 294
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 240 SITDNFQVIFDGNANWEAAQA---QGGAICC--TTTDKTVTLTGNKLSFTNNALT 292
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 295 GGAIYVKKLELASGLTLFSRNSVNGTAPK--GGAIATEDSGELISADSGDIVFLGNT 352
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 293 GGAIISGLKVSISAGPPTLFQSN-1SGSAGOGGGGAINIASAGELALSATSGLDITFNNQ 351
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 353 VTSTTPGNNRSSIDLGTSAKMTALRSAGRAIYFYDPTTSGSTVTVDLVKVNTPADSA 412
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 352 VTNGSTST-RNAINIIDTAKVTSIRATGQSIYFYDPTTNPCTAASDTTLNLNADANSE 410
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 413 LQYTGNIIFTGKLESEADSKNLTSLKLOPVTLSGGTSLSKHGVTLTQTAFTQADSR 472
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 411 IEYGAIIVFSGEKLSPTEKALAAVNTSIROPVAVLARGDLVLRDGVTVTFKDLTQSPGR 470
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 473 LEMDVGTTLEPADTS-TNNIVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTF 531
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 471 ILMDDGTTLSAKEANLSGLAVNLSSLDGNTKAALKTEAADKNLSLSTIALIDTEGSF 530
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 532 YENHSLRNPOQSDILELK---ASGTVTSTAVTPDPIMGEKHYGQGTGWGPIVWGTGAST 588
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 531 YENHNLKSASTYPLLELTTAGANGTITLGAALSTLTLPBETHYGYQGNW-QLSWANATSS 589
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 589 -TATFNWTKTGIVNPERIGSLVPSNLSMNAFIDISSLHVMETANEGLQGDRAFWCAGLS 647
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 590 KIGSINWRTGTVIPSERKSNLPLNSLWGNFIDIRSIQLIETKSSGEPFERELWLSGIA 649
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 648 NFFHKDSTKTRRGFRHLGGVIGVGNLHTCDKILSAAFCOLFGRDRDRYFVAKNQGTVYG 707
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 650 NFFYRDSMPTRHGFRHISGGYALGITATTPAEDQLTFAFCQLFARDNRHITGKNHGDYV 709
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 708 GTLYVQHNETYISLPCKL-----RPSLSVYVPTPIVLFSGNLSTYTHDNDLTKYTTY 761
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 710 ASLYPHHTEGLEGLFDIANFLWGKATRAPWVLSLSQIIPLSFADKFSYLHTDNHMKTYTND 769
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 762 PTVKSGWGNDSFALFEGGRAPICLDESALFEQYMPFMKLQFYAHQEGFKEQGTAREFG 821
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 770 SIIKGSWRNDAFCADLGASLPVIVSVPYLLKEVEFPVKVQYIYAHQQDFYERHAEGRAPN 829
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 822 SSSLNVALPIGIREDKESDCODATYNLTGYTDLVRSNPDCTTLTIRSGDSMKTFTGN 881
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 830 KSELINVEIPIGTVTERDSKSEKGYDITLMYILDAYRNPCKQTSLIASDANWYAGTN 889
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY 882 LARQALVLRAGNHFCNFSNFEAFSOFPELGRSSRNYNVDLGAKYQF 928
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 890 LARQGFVSRAANHFOVNPHMEIFGQFAFEVRSRNRNNTNLGSKFCF 936
| | | | | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 9
US-10-312-273-153
; Sequence 153, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
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[illegible]

RESULT 11

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RESULTS 11
US-10-324-129-4
; Sequence 4, Application US/10324129
; Publication NO. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 925
; TYPE: prt
; ORGANISM: Chlamydia pneumoniae
US-10-324-129-4

```

	Query Match	40.8%;	Score	1946.5;	DB	14;	Length	925;
	Best Local Similarity	43.5%;	Pred.No.	6.9e-137;				
	Matches	404;	Conservative	177;	Mismatches	319;	Indels	29; Gaps
								15;
Qy	18	LSMIATETVLDS--ASPDGKNGKNFNSVRESQE-DAGTTFYLFKGNVLTLENIPGTGTAITS	75					
Dd	8	LSIVAAEVTLLDSNNNSVDGGNGTTFTVFSTDDAAGTYSLLSDVSFNAGALCIPLASG	67					

RESULT 12

```

RES001.12
US-10-289-762-470
; Sequence 470, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, thereof and uses thereof, in particular for the diagnosis and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27

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; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-470

Query Match      40.6%; Score 1940; DB 15; Length 930;
Best Local Similarity 43.7%; Pred. No. 2.1e-136;
Matches 416; Conservative 165; Mismatches 324; Indels 48; Gaps 17;

QY 1 MKSSPKFVFSTPAIFPLSM-IAT---ETVLDSSASFQGNKGNFVSRESQEDAGTTLF 56
Db 1 MKIPLHKLIISSLTVPILLIATYGDASLSPTDSFDGAGGSTFTPKSTADANGTNYVL 60

QY 57 KGNVTLNIPGTCGTATKSCFNNTKGLTFTGNSLLPOTVDAGTVAGAAVNSVVVDKS 116
Db 61 SGNVYI-NDAGKGTALTGCCFTTGDLTFTGKGYFSFNTVDAGNAGAAA-SITADKA 118

QY 117 TTFIGFSSLSFIASPGSSITTKGAVSCSTGSLTKNVSLFSSKNFSTD---NGGAI 173
Db 119 LFTFGFNSLFIAPGTTVASGKSTLS-SAGALNTDNGTILFQNSVNEANNNGAIT 177

QY 174 KTLSTLTGTTMSALFSENTSSKGGAIQTSDALITGNOQEVFSFSDSSDGAIFTEAS 233
Db 178 KTLISGNTSSITFTSNSAKLGGAIYSSAAASISGNTGQVFMNKGTTGGGALGF 237

QY 234 VTISNNAKVSFIDNKVTGASSSTTGDMSCGAIKAYKTSTDTKTLTGNOMLF 293
Db 238 SSITQNSLFFSGNTATDAAG-----KGGAIYCEKGTGTPPTLTISGNSLTFA 291

QY 294 AGGAIYVKKLELASGLLTFRSNVNGGTAPKGAIAIEDSGELSLSDSGDITVFLG 353
Db 292 QGGAICAHGLDLSAAGPTLFSNNRCNTAAGKGAIAIADSGSLSANQGDITFLGN 351

QY 354 TSTT-PGTRNSSIDLTSAMTALRSAGRAIYFYDPI---TTGSSFTVDVLKVN 409
Db 352 TSTSAPTSTRNAILYLGSSAKITNLRAAQGSIFYDPIASNTTGAS---DVLTI 407

QY 410 DSNALQVTGNLITGKLSLSEADSKNLSKLIQPTVLSGTLKXHGVTLOQTAA 469
Db 408 NSPLDYSGTIVFSGEKLSEADSKNLSKLIQPTVLSGTLKXHGVTLOQTAA 467

QY 470 DSRLEMDVGTLEPADTSTIN--NLVINTSSIDGAKKAKIETKATSKNLTSL 527
Db 468 GSTLLMQPGTKLK-AUTEALSLTKLVLDLSALEGKSVSLETAGANKTILTS 526

QY 528 TGTFTYENHSLRNPQSDYDILELKAS-----GTVTSTAVTPDPIMGEKPHY 578
Db 527 SGNFYESHNTINQAFQPLVVFVTAATAASDIYIDALLTSPVQTPDEP----- 580

QY 579 PIVWGTGASTTATFNWTKGYINPERIGSLVPSNLWNAFIDISLHYLMETANE 638
Db 581 ATWADTSTAKSGTMTWTTGYNPNERRASVWPSLWASFTDRTIQQIMTSQANS 640

QY 639 RAFPWAGLNFHFKDSTKRRGRPHRLSGGVIYGNLHNTCSDKILSAACOLFORD 698
Db 641 RGLWASGTANFHKDKSGTNOAFRHKSXYGIYVGSRAEDFSENIFSVAFCOLF 700

QY 699 AKNQGTIVYGTLYYQHNETYISLPCKLKRPC--SLSYVPTPIVLFSGNLSYTH 756
Db 701 VENTSHNYLASLYLQHRFLGGLP--MPSFGSITDMLKDIPILNAQLSISYTK 757

QY 757 KYTTYTVVGSWNDSFALFEGGRAPICL-DESALFEQYPMFKLQFVIAHQBP 815
Db 758 RYTSYPEAQSGTWNNSGALGSLALYLPKEAPFFQGFYFPLKFOAVYSRQNF 817

QY 816 EAREFGSSRLNALPIGIRFDKESQDQATYNLTIGYTVDLVRSPDCDTTLIR 875
Db 818 EARAFTDGLVNCISIPVGIHLEKISDEKKNFISLAYIGDVYRKPRRTSLMV 877

QY 876 KTGTTNLARQALVLRAGNHFCFNSNFAPFSQPSFELRGSSRNYNVDLGAKY 928
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Db 878 TSLCKNLARQAFPLASAGSHLTLSPHVELSGEAYELRGSAAHYNVDCGLRYSF 930

RESULT 13
US-10-282-122A-54680
; Sequence 54680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54680
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54680

Query Match      40.6%; Score 1936; DB 12; Length 930;
Best Local Similarity 43.5%; Pred. No. 4.2e-136;
Matches 415; Conservative 165; Mismatches 325; Indels 48; Gaps 17;

QY 1 MKSSPKFVFSTPAIFPLSM-IAT---ETVLDSSASFQGNKGNFVSRESQEDAGTTLF 56
Db 1 MKIPLHKLIISSLTVPILLIATYGDASLSPTDSFDGAGGSTFTPKSTADANGTNYVL 60

QY 57 KGNVTLNIPGTCGTATKSCFNNTKGLTFTGNSLLPOTVDAGTVAGAAVNSVVVDKS 116
Db 61 SGNVYI-NDAGKGTALTGCCFTTGDLTFTGKGYFSFNTVDAGNAGAAA-SITADKA 118

QY 117 TTFIGFSSLSFIASPGSSITTKGAVSCSTGSLTKNVSLFSSKNFSTD---NGGAI 173
Db 119 LFTFGFNSLFIAPGTTVASGKSTLS-SAGALNTDNGTILFQNSVNEANNNGAIT 177

QY 174 KTLSTLTGTTMSALFSENTSSKGGAIQTSDALITGNOQEVFSFSDSSDGAIFTEAS 233
Db 178 KTLISGNTSSITFTSNSAKLGGAIYSSAAASISGNTGQVFMNKGTTGGGALGF 237
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Qy 234 VTISNNAKVSFIDNKVGTGASSSTTGDMSGGAICAYKTSITDTKVTLTGNQMLLFNSNTSTT 293
Db 238 SSITQNSLSPFSGNTATDAAG-----KGGAIYCEKGETPTLTISGNKSLTFAENSVT 291
Qy 294 AGGAIYVKLELASGGLTLPSRNSVNGTAPKGGAIATIEDSGELSLSDSDGIVFLGNVT 353
Db 292 QGGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIATADSGSLSANQGDITFLGNLT 351
Qy 354 TSTT-PGTRNSRIDLTSKMTALRSAGRAIYFYDPI---TTGSSTTTVDLVKVNTPA 409
Db 352 TSTGAPTSTRNAILYVGSAGKITNLRAGQGGIYFYDPIASNTTAS-----DVLINQPD 407
Qy 410 DSALQYTGNIIFTGKELSETAADSKNLTKLQPVTLSSGGLSLKHGVTLTQTAFTQA 469
Db 408 NSPLDYSGTIVFSGEKLSDAEKADNFTSLKQPLALASGTLAKGNVELDVNGFTQTE 467
Qy 470 DSRLEMDVGTLEPADTSTIN--NLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDP 527
Db 468 GSTLLMQPGTKLK-ADTEAISLTKLVDLSALEGNKSVSIETAGANKTITLTSPLVFQDS 526
Qy 528 TGTFFYENHSLRNPOSYDILELKAS-----GTVTSTAVTPDPIMGEKPHYGYQGTWG 578
Db 527 SGNFYESTINQAFTQPLVWFTATAASDIYDALLTSPVQTPEP-----HYGYQHWE 580
Qy 579 PIVMGTGASTTATFNWTKTYIPNPERIGSLVPNSLWNAFIDISLHYLMETANEGLQGD 638
Db 581 ATWADTSTAAGTMTWVTGYNPNPERRASVVPDLSWASFTDIRTLOQIMTSQANSIYQ 640
Qy 639 RAFWCAGLSNFHKDSTKTRGFRHLSCGYVIGGNLHCTCDKILLSAAFCOLFGRRDRYFV 698
Db 641 RGLWASGTANFHKDKSGTNOAFRHKSYGYIVGSAEDFSENIFSVAFCOLFGKDKDLFI 700
Qy 699 AKNQTVGGTLYYQHNETYISLPCKLKRPC--SLSYVTEIPVLPFSGNLSYTHTDNDLKT 756
Db 701 VENTSHNYLASLYLQHRFLGGLP---MPSFGSITDMLKDPIILNAQLSYTKNDMDT 757
Qy 757 KYTTYPTVKSGWNGDSFALEFGGRAPICL-DESALFEQYMPFMKQFYVAHQEGKEQGT 815
Db 758 RYTSYPEAQGSWTNNSGALGGLSLALYLPKEAPFFQGYFFFLKFPQAVYSRQONKESGA 817
Qy 816 BARFSGSRNLNLAIPGIRFDKESDCQDATYNLTGLYTVDLVRNPNPCTTTLRISGDSW 875
Db 818 EARAFDDGDLVNCISIPVGRLEKISEDEKNFELSLAYIGVYRKNPRSRSLMVSGASW 877
Qy 876 KTFGTGNLARQALVIRAGNHFCNSNFEAFSPFELGRSGSRNRYNDLGAQYQF 928
Db 878 TSLCKNLARQALASAGSHLTLSPHVELSGEAAYELRGAHLYNVDCGLRYSF 930
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RESULT 14

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US-10-312-273-45
; Sequence 45, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
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; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 45
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-45
```

```
Query Match 40.6%; Score 1936; DB 15; Length 930;
Best Local Similarity 43.5%; Pred. No. 4.2e-136; Indels 48; Gaps 17;
Matches 415; Conservative 165; Mismatches 325;
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Qy 1 MKSFPKVFSTFAIFPLSM-IAT---ETVLDSASSFDGNKNGNFSVRESQEDAGTYYLF 56
Db 1 MKIPLHKLILSSITLVTPILLSIATYGADASLSPDSDPDGAGGSTFTPKSTADANGTNVVL 60
Qy 57 KGNVTLENIPOTGTAIYKSCFNNTKGLDITFTGNGNSLLFPQTVADGTAGAAVNSVVDKS 116
Db 61 SGNVYI-NDAGKGALTGCCFTETTTGDLTFTGKGYFSFNTVDAGSNAGAAA-SFTADKA 118
Qy 117 TTRTGFSLSPFIASPGSSITTTGKAVSCSTGSLSI-TKNVSLLSFKNPSD--NGCALTA 173
Db 119 LTFTGFNSLSIAAPGTVIAGSKSTLS-SAGALLNTDNGTILFSGVNSNEANNNGAITYT 177
Qy 174 KTLSTGTMTBMALEFSENTSSKKGAIQTSDALITITGNQGVSVFSFSDNTSSDGAALIFTRAS 233
Db 178 KTLISGNTSITFTSNAKKGAIYSSAASISGNTGQLVFEMNKGETGGALGFEEAS 237
Qy 234 VTISNNAKVSFIDNKVGTGASSSTTGDMSGGAICAYKTSITDTKVTLTGNQMLLFNSNTSTT 293
Db 238 SSITQNSLSPFSGNTATDAAG-----KGGAIYCEKGETPTLTISGNKSLTFAENSVT 291
Qy 294 AGGAIYVKLELASGGLTLPSRNSVNGTAPKGGAIATIEDSGELSLSDSDGIVFLGNVT 353
Db 292 QGGAICAHGLDLSAAGPTLFSNNRCGNTAAGKGGAIATADSGSLSANQGDITFLGNLT 351
Qy 354 TSTT-PGTRNSRIDLTSKMTALRSAGRAIYFYDPI---TTGSSTTTVDLVKVNTPA 409
Db 352 TSTGAPTSTRNAILYVGSAGKITNLRAGQGGIYFYDPIASNTTAS-----DVLINQPD 407
Qy 410 DSALQYTGNIIFTGKELSETAADSKNLTKLQPVTLSSGGLSLKHGVTLTQTAFTQA 469
Db 408 NSPLDYSGTIVFSGEKLSDAEKADNFTSLKQPLALASGTLAKGNVELDVNGFTQTE 467
Qy 470 DSRLEMDVGTLEPADTSTIN--NLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDP 527
Db 468 GSTLLMQPGTKLK-ADTEAISLTKLVDLSALEGNKSVSIETAGANKTITLTSPLVFQDS 526
Qy 528 TGTFFYENHSLRNPOSYDILELKAS-----GTVTSTAVTPDPIMGEKPHYGYQGTWG 578
Db 527 SGNFYESTINQAFTQPLVWFTATAASDIYDALLTSPVQTPEP-----HYGYQHWE 580
Qy 579 PIVMGTGASTTATFNWTKTYIPNPERIGSLVPNSLWNAFIDISLHYLMETANEGLQGD 638
Db 581 ATWADTSTAAGTMTWVTGYNPNPERRASVVPDLSWASFTDIRTLOQIMTSQANSIYQ 640
Qy 639 RAFWCAGLSNFHKDSTKTRGFRHLSCGYVIGGNLHCTCDKILLSAAFCOLFGRRDRYFV 698
Db 641 RGLWASGTANFHKDKSGTNOAFRHKSYGYIVGSAEDFSENIFSVAFCOLFGKDKDLFI 700
Qy 699 AKNQTVGGTLYYQHNETYISLPCKLKRPC--SLSYVTEIPVLPFSGNLSYTHTDNDLKT 756
Db 701 VENTSHNYLASLYLQHRFLGGLP---MPSFGSITDMLKDPIILNAQLSYTKNDMDT 757
Qy 757 KYTTYPTVKSGWNGDSFALEFGGRAPICL-DESALFEQYMPFMKQFYVAHQEGKEQGT 815
Db 758 RYTSYPEAQGSWTNNSGALGGLSLALYLPKEAPFFQGYFFFLKFPQAVYSRQONKESGA 817
Qy 816 BARFSGSRNLNLAIPGIRFDKESDCQDATYNLTGLYTVDLVRNPNPCTTTLRISGDSW 875
Db 818 EARAFDDGDLVNCISIPVGRLEKISEDEKNFELSLAYIGVYRKNPRSRSLMVSGASW 877
Qy 876 KTFGTGNLARQALVIRAGNHFCNSNFEAFSPFELGRSGSRNRYNDLGAQYQF 928
Db 878 TSLCKNLARQALASAGSHLTLSPHVELSGEAAYELRGAHLYNVDCGLRYSF 930
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QY 876 KTGTTNLRQALVLRAGNHFCFNSNFEPASQSFELRGSSRNVNVDLGAKYQF 928

Db 878 TSLCKNLRQAFILASAGSHLITLSPHVELSGEAAEYELRGSAHTNVNDCGLRYGSF 930

RESULT 15

US-10-289-762-472
; Sequence 472, Application US/10289762
; Publication No. US20040006218A1

: GENERAL INFORMATION:

APPLICANT: Griffais. R.

; AFFILIANTI: GILLIGIS, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and tre

FILE REFERENCE: 9710-003-999

: CURRENT APPLICATION NUMBER: IIS/1

CURRENT FILING DATE: 2003

; CURRENT FILLS
; NUMBER OF SECS

; NUMBER OF SEQ

; SEQ ID NO 41

; LENGTH: 927

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; TYPE: PR

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ORGANISM: *Chlamydomonas reinhardtii*

FEATURE:

FEATURE:	NAME/KEY:	STTF
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; NAME/KEY: STI
LOCATION: 1

Query Match	40.2%	Score 1917.5;	DB 15;	Length 927;
Best Local Similarity	44.8%	Pred. No. le-134;		
Matches 427;	Conservative 147;	Mismatches 328;	Indels 51;	Gaps 22;

E4 VI EVANGELIUM ENTI DOCTORE ET HUIUS COMMUNITATIS BENEFICENTIA

114 DKSTTFEGPSSI.SET ASDGSSITTTCKKAYSCGTCSEI SITWYVSI I ESKNPESTDNCCITTA 173

OV 174 KTI,SI,TGTTMSAI,FSENTSSKKGGA,TOTSDAI,TITGNOGEVSEFSDNTSSDSSGAA,TFTTAS 233

QV 234 VTISNNAKVSEFIDNKVVTGASSSTGDMSSGGAICAYKTSTDTKV-TLTGNOMLLESNNTST 292

Qy 293 TAGGAIYVKKLELASGGLTLFSRNSVNGGTAPKGGAI AIEDSGELSL SADSADSGDIVFLGNT 352

QY 353 V---TSTTGTNRSSIDLG-TSAKMTALRSAAGRAIYFYDPITTTGSSTTVTVDVLKVNETP 408

QY 409 ADSALQYTGNIIFTGEKLSETEAADSKNLTSKLLQPVTLSSGGLSLKHGVTLQTQAFQQ 468

QY 469 ADSRLEMDVGTLEPADTSTINNLVINISSIDGAKKAKIET-KAT--SKNLTLSGTITLL 525

QY 526 DPTGTFYENHSLRNPQSYDILELKAS--GTVTSTAVTPDPIMGEKFHYGYQGTWGPIVWG 583

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 13:06:40 ; Search time 58 seconds
(without alignments)
4520.760 Million cell updates/sec

Title: US-09-428-122-2

Perfect score: 4774

Sequence: 1 MKSFFPKFVSTFAIFPLSM.....PELGRSRNVNVLGAKYQF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4774	100.0	928	3	AAY94327 Chlamydia
2	4760	99.7	928	2	AAW88421 Chlamydia
3	3865	81.0	746	5	ABB90535 Chlamydia
4	2802.5	58.7	597	2	AAY34611 Chlamydia
5	2058	43.1	928	2	AAW88418 Chlamydia
6	2048	42.9	928	5	ABB90573 Chlamydia
7	2021	42.3	928	3	AAY90237 Chlamydia
8	2006	42.0	918	3	AAY69369 Amino aci
9	2001	41.9	918	2	AAW88422 Chlamydia
10	1993	41.7	914	2	AAW88429 Chlamydia
11	1987.5	41.6	885	3	AAY90238 Chlamydia
12	1986	41.6	928	2	AAW88423 Chlamydia
13	1982	41.5	928	5	ABB90542 Chlamydia
14	1976	41.4	928	3	AAY90239 Chlamydia
15	1965	41.2	936	3	AAY99842 Chlamydia
16	1965	41.2	936	5	ABB90602 Chlamydia
17	1965	41.2	936	6	ABU26755 Protein e
18	1946.5	40.8	925	3	AAY99843 Chlamydia
19	1940	40.6	930	2	AAAY35052 Chlamydia
20	1936	40.6	930	5	ABB90548 Chlamydia
21	1936	40.6	930	6	ABU26756 Protein e
22	1930	40.4	930	3	AAY90240 Chlamydia
23	1927	40.4	930	2	AAW88424 Chlamydia
24	1917.5	40.2	927	2	AAY35054 Chlamydia
25	1915	40.1	926	5	ABP56019 Chlamydia

26	1915	40.1	926	5	ABB98228 Chlamydia
27	1915	40.1	926	6	ABU6284 C. psitt
28	1856	38.9	949	2	AAW88417 Chlamydia
29	1855	38.9	928	2	AAW88417 Chlamydia
30	1855	38.9	928	3	AAAY90236 Chlamydia
31	1855	38.9	928	5	ABB90583 Chlamydia
32	1855	38.9	928	6	ABU26757 Protein e
33	1832	38.4	945	3	AAW88428 Chlamydia
34	1811	37.9	945	2	AAW88428 Chlamydia
35	1656.5	34.7	839	5	ABP56002 Chlamydia
36	1656.5	34.7	839	5	ABB98211 Chlamydia
37	1656.5	34.7	839	6	ABU62677 C. psitt
38	1573	32.9	841	5	ABB90595 Chlamydia
39	1573	32.9	841	6	ABU26753 Protein e
40	1572.5	32.9	643	2	AAAY35056 Chlamydia
41	1570	32.9	841	3	AAAY92818 C. pneumo
42	1564	32.8	841	2	AAW88420 Chlamydia
43	1442.5	30.2	922	5	ABB90546 Chlamydia
44	1437.5	30.1	922	3	AAAY95548 Chlamydia
45	1430.5	30.0	922	2	AAW88419 Chlamydia

ALIGNMENTS

RESULT 1

AAY94327
ID AAY94327 standard; protein; 928 AA.

XX AC AAY94327;

XX AC

DT 12-SEP-2003 (revised)

DT 11-AUG-2000 (first entry)

XX DE Chlamydia pneumoniae 98kD putative outer membrane protein.

XX KW Chlamydia; antigen; vaccine; infection; outer membrane protein.

XX OS Chlamydia pneumoniae.

XX OS Chlamydia pneumoniae.

XX PN WO200026237-A2.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-GB003579.

XX PR 29-OCT-1998; 98US-0106070P.

XX PR 01-MAR-1999; 99US-0122066P.

XX PR 27-OCT-1999; 99US-00428122.

XX (CONN-) CONNAUGHT LAB LTD.

XX Murdin AD, Oomen RP, Dunn PL;

XX N-PSDB; AAA27021.

XX WPI; 2000-365569/31.

XX Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for

XX vaccination and protection against Chlamydia infection.

XX Claim 6; Fig 1; 93pp; English.

XX The present sequence is the 98kDa putative outer membrane protein from

XX Chlamydia pneumoniae. The genomic sequence was amplified using two PCR

XX primers. The 5' primer contains a NotI restriction site, a ribosome

XX binding site, an initiation codon and a sequence close to the 5' end of

XX the 98kDa putative outer membrane protein coding sequence. The 3' primer

XX contains the sequence encoding the C-terminal sequence of the putative

XX outer membrane protein and a BglI restriction site. The stop codon was

XX excluded and an additional nucleotide was inserted to obtain an in-frame

XX C-terminal fusion with the Histidine tag. The PCR product was cloned into

XX a eukaryotic expression vector (pCA-Myc-His) by restricting both the

XX vector and the PCR product with NotI and BamHI and performing a ligation

CC reaction. This expression vector was injected intramuscularly and
CC intranasally into mice, which were subsequently inoculated with Chlamydia
CC pneumoniae. The chlamydial lung titers of the immunised mice were lower
CC than those of the controls. Thus the 98kDa putative outer membrane
CC protein can be used as a vaccine to provide protection against Chlamydia
CC infections, especially Chlamydia pneumoniae infections. The present
CC polypeptide may also be administered orally to treat Chlamydia infection.
CC (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 928 AA;

Query Match 100.0%; Score 4774; DB 3; Length 928;
Best Local Similarity 100.0%; Pred. No. 5.7e-307;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSSFPKVFSTFAIFPLSMIATETVLDSSASFDGKNGNFSVRSQEDAGTYLFGKV 60
DB 1 MKSSFPKVFSTFAIFPLSMIATETVLDSSASFDGKNGNFSVRSQEDAGTYLFGKV 60
QY 61 TLENIPGTGTAITKSCFNNTKGLTFTGNGNLLFTQVDAGTVAGAAVNSSVVDKSTTFI 120
DB 61 TLENIPGTGTAITKSCFNNTKGLTFTGNGNLLFTQVDAGTVAGAAVNSSVVDKSTTFI 120
QY 121 GFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSLLFSKNFSTDNGGAI TAKTLSLTG 180
DB 121 GFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSLLFSKNFSTDNGGAI TAKTLSLTG 180
QY 181 TTMSALFSENTSSKGGAIQTSDALITGNOQEVFSFSDNTSSDGAIFTEASVTISNNA 240
DB 181 TTMSALFSENTSSKGGAIQTSDALITGNOQEVFSFSDNTSSDGAIFTEASVTISNNA 240
QY 241 KVSFIDNKVTGASSSTTGDMGGAI CAYKTSITDTKVTLTGNOMLLFSNNSTTTAGGAIYV 300
DB 241 KVSFIDNKVTGASSSTTGDMGGAI CAYKTSITDTKVTLTGNOMLLFSNNSTTTAGGAIYV 300
QY 301 KKLEASGGLTLFNRNSVNGTAPKGGAI AIEDSGBELSLADSGDVI VFLGNVTSTTPTGT 360
DB 301 KKLEASGGLTLFNRNSVNGTAPKGGAI AIEDSGBELSLADSGDVI VFLGNVTSTTPTGT 360
QY 361 NRSSIDLGTSAKMTALRSAGRAIYFDPITGSSVTVDVLKVNTPADSALQYTGNI 420
DB 361 NRSSIDLGTSAKMTALRSAGRAIYFDPITGSSVTVDVLKVNTPADSALQYTGNI 420
QY 421 FTGEKLSEADSKNLTSLKLPVTLSGGTL SLKHGVTIQTQAFQQADSRLEMDVGT 480
DB 421 FTGEKLSEADSKNLTSLKLPVTLSGGTL SLKHGVTIQTQAFQQADSRLEMDVGT 480
QY 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTFYENHSLRNP 540
DB 481 LEPADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTFYENHSLRNP 540
QY 541 QSYDILELKASGTVTSTAVTPDPIMGEKHYGQGTWGPVWGTVGASTTATFNWTKGYI 600
DB 541 QSYDILELKASGTVTSTAVTPDPIMGEKHYGQGTWGPVWGTVGASTTATFNWTKGYI 600
QY 601 PNERIGSLVPNSLWNAFIDISSILHYMETANEGLOQDRAFWCAGLSNFFPKDSTKTRRG 660
DB 601 PNERIGSLVPNSLWNAFIDISSILHYMETANEGLOQDRAFWCAGLSNFFPKDSTKTRRG 660
QY 661 FRHLGGYVIGGNLHTCSDKILSAAPCOLFRGRDRDVFVAKNQGTGTYGTYQHNETYIS 720
DB 661 FRHLGGYVIGGNLHTCSDKILSAAPCOLFRGRDRDVFVAKNQGTGTYGTYQHNETYIS 720
QY 721 LPCKLRCSLSYVPTETPVLPSGNLSYTHTDNDLTKYTYPTVKSGWGNDSFALEFGGR 780
DB 721 LPCKLRCSLSYVPTETPVLPSGNLSYTHTDNDLTKYTYPTVKSGWGNDSFALEFGGR 780
QY 781 APICLDESALFEQWPMFKLQFYVAHQEGFKEQGTAREFGSSRLVNLALPIGIRFDKES 840
DB 781 APICLDESALFEQWPMFKLQFYVAHQEGFKEQGTAREFGSSRLVNLALPIGIRFDKES 840
QY 841 DCQDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKTFGTNLARQALVLRAGNHFCFNSN 900
DB 841 DCQDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKTFGTNLARQALVLRAGNHFCFNSN 900

DB 841 DCQDATYNLTGYTVDLVRSNPDCTTTLRISGDSWKTFGTNLARQALVLRAGNHFCFNSN 900
QY 901 FEARSQSFELRGSSRNYNVDLGAKYQF 928
DB 901 FEARSQSFELRGSSRNYNVDLGAKYQF 928
RESULT 2
AAW88421
ID AAW88421 standard; protein; 928 AA.
XX AAW88421;
AC AAW88421;
XX 17-OCT-2003 (revised)
DT 26-APR-1999 (first entry)
DE Chlamydia pneumoniae surface exposed protein Omp8.
XX Omp8; outer membrane protein 8; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma.
XX Chlamydia pneumoniae.
XX WO9858953-A2.
XX 30-DEC-1998.
XX 19-JUN-1998; 98WO-DK0000266.
XX 23-JUN-1997; 97DK-00000744.
XX (BIRK/) BIRKELUND S.
XX (CHRI/) CHRISTIANSEN G.
XX Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
WPI; 1999-105610/09.
DR N-PSDB; AAX06820.
XX Species-specific test for identifying mammals infected with Chlamydia
PT pneumoniae - comprises detecting antibodies specific for outer membrane
PT proteins of C. pneumoniae or nucleic acids encoding these proteins.
XX Claim 7; Page 53-55; 115pp; English.
XX This polypeptide comprises the novel 90.0 kDa surface exposed protein
CC Omp8 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
CC acid sequence was deduced from DNA (see AAX06820) isolated from a C.
CC pneumoniae expression library. The invention provides 12 novel surface
CC exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid
CC sequences encoding them (see AAX06816-27). A new species specific test is
CC claimed that is used to identify mammals (including humans) infected with
CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
CC proteins can also be used in the immunization of mammals, the nucleic
CC acids being particularly useful as DNA vaccines for effecting in vivo
CC expression of antigens. The vaccines may also prevent atherosclerosis and
CC bronchial asthma, which are possibly associated with C. pneumoniae.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 928 AA;

Query Match 99.7%; Score 4760; DB 2; Length 928;
Best Local Similarity 99.7%; Pred. No. 4.8e-306;
Matches 925; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKSSFPKVFSTFAIFPLSMIATETVLDSSASFDGKNGNFSVRSQEDAGTYLFGKV 60
DB 1 MKSSFPKVFSTFAIFPLSMIATETVLDSSASFDGKNGNFSVRSQEDAGTYLFGKV 60
QY 61 TLENIPGTGTAITKSCFNNTKGLTFTGNGNLLFTQVDAGTVAGAAVNSSVVDKSTTFI 120

Db 61 TLEIPGTAITKSCFNNTKGLTFTGNGSLLFQTVDAGTVAGAAVSSVVDKSTTFI 120
Qy 121 GFSSLSFTASPGSSITTCGKAVSCSTGSLTKNVLFSKNFSDNGGAIKAKTILSLTG 180
Db 121 GFSSLSFTASPGSSITTCGKAVSCSTGSLTKNVLFSKNFSDNGGAIKAKTILSLTG 180
Qy 181 TMSALFSENTSSKKGGAIQTSALITITNGQEVFSFSDNTSSDGAALFTEASVTISNNA 240
Db 181 TMSALFSENTSSKKGGAIQTSALITITNGQEVFSFSDNTSSDGAALFTEASVTISNNA 240
Qy 241 KVSFIDNKVTCASSSTTGDMSGGAICAYKTDKVTITGNQMLLSFNSNTTTAGGAIYV 300
Db 241 KVSFIDNKVTCASSSTTGDMSGGAICAYKTDKVTITGNQMLLSFNSNTTTAGGAIYV 300
Qy 301 KKLASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPTG 360
Db 301 KKLASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPTG 360
Qy 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGSTTVDVLKVNTPADSALOYTGNI 420
Db 361 NRSSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGSTTVDVLKVNTPADSALOYTGNI 420
Qy 421 FTGKLSSETAADSKNLTSKLLQVTLSSGTLSLKHGVTLOTAFTQOADSRLMDVGT 480
Db 421 FTGKLSSETAADSKNLTSKLLQVTLSSGTLSLKHGVTLOTAFTQOADSRLMDVGT 480
Qy 481 LEPADTSTINNLVINISIDGAKKAKETKATSKNLTLSGTITLDDPTGFYENHSLRNP 540
Db 481 LEPADTSTINNLVINISIDGAKKAKETKATSKNLTLSGTITLDDPTGFYENHSLRNP 540
Qy 541 QSDIILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTVGASTTATFNWTKGYI 600
Db 541 QSDIILELKASGTVTSTAVTPDPIMGEKPHYGYQGTWGPVWGTVGASTTATFNWTKGYI 600
Qy 601 PNERIGSLVPSNLWNAFIDISSILHYMETANEGLQDRAFWCAGLSNPFHKDSTKTRRG 660
Db 601 PNERIGSLVPSNLWNAFIDISSILHYMETANEGLQDRAFWCAGLSNPFHKDSTKTRRG 660
Qy 661 FRHLSGGYVIGGNNLHTCSDKILSAFCQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYIS 720
Db 661 FRHLSGGYVIGGNNLHTCSDKILSAFCQLFGRDRDYFVAKNQGTVYGGTLYYQHNETYIS 720
Qy 721 LPCKLRPCSLSYVPTPIVPSGNLSYTHDNDLTKYTYPTVKGSGNDSFALFEGGR 780
Db 721 LPCKLRPCSLSYVPTPIVPSGNLSYTHDNDLTKYTYPTVKGSGNDSFALFEGGR 780
Qy 781 APICLDESALFEQYMPKMLQFYVAHQEGFKEQTEAREFGSSRLVNLALPIGIRFDKES 840
Db 781 APICLDESALFEQYMPKMLQFYVAHQEGFKEQTEAREFGSSRLVNLALPIGIRFDKES 840
Qy 841 DCQDATYNTLGYTVDLVRNPNCTTTLRISGDSWKTFGTLNARQALVLRAGNHFCFNSN 900
Db 841 DCQDATYNTLGYTVDLVRNPNCTTTLRISGDSWKTFGTLNARQALVLRAGNHFCFNSN 900
Qy 901 FEAFSOFSELPGRSSRNYNVDLGAQYQF 928
Db 901 FEAFSOFSELPGRSSRNYNVDLGAQYQF 928

RESULT 3

AB990535
ID ABB90535 standard; protein; 746 AA.

XX ABB90535;

XX 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)

XX Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;

coronary artery disease; carotid artery stenosis; myocardial infarction;
cerebrovascular disease; aortic aneurysm; claudication; stroke;
strain CML029.

Chlamydia pneumoniae.

WO200202606-A2.

10-JAN-2002.

03-JUL-2001; 2001WO-IB001445.

03-JUL-2000; 2000GB-00016363.

11-JUL-2000; 2000GB-00017047.

21-JUL-2000; 2000GB-00017983.

07-AUG-2000; 2000GB-00019368.

18-AUG-2000; 2000GB-00020440.

14-SEP-2000; 2000GB-00022583.

10-NOV-2000; 2000GB-00027549.

22-DEC-2000; 2000GB-00031706.

(CHIR-) CHIRON SPA.

Ratti G, Grandi G;

WPI: 2002-154726/20.

N-PSDB; ABL91193.

Novel Chlamydia pneumoniae protein useful in the manufacture of a
medicament for treatment or prevention of infection due to Chlamydia,
preferably Chlamydia pneumoniae, and for diagnostic purposes.

Claim 1; Page 49-50; 364pp; English.

Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
them. The proteins are predicted to be immunogenic and may therefore be
useful in vaccine production and for diagnostic purposes. Chlamydia
pneumoniae is a common cause of respiratory disease in humans, and is
also involved in the development of cardiovascular diseases such as
atherosclerosis, coronary artery disease, carotid artery stenosis,
myocardial infarction, cerebrovascular disease, aortic aneurysm,
claudication and stroke. The proteins and nucleic acids of the invention
may be used in vaccines and pharmaceutical compositions for the
prevention or treatment of chlamydial infections, particularly Chlamydia
pneumoniae infections. The proteins may also be used in the detection of
Chlamydia pneumoniae, and the nucleic acids may be used in the detection of
DNA probe assay or blotting techniques for determining Chlamydia
pneumoniae gene expression. The present sequence represents a
specifically claimed Chlamydia pneumoniae protein of the invention.

(Updated on 29-AUG-2003 to standardise OS field)

Sequence 746 AA;

Query Match 81.0%; Score 3865; DB 5; Length 746;
Best Local Similarity 100.0%; Pred. No. 5.9e-247; Gaps 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0;

Qy 183 MSALFSENTSSKKGGAIQTSALITITNGQEVFSFSDNTSSDGAALFTEASVTISNNAKV 242
Db 1 MSALFSENTSSKKGGAIQTSALITITNGQEVFSFSDNTSSDGAALFTEASVTISNNAKV 60
Qy 243 SFIDNKVTCASSSTTGDMSGGAICAYKTDKVTITGNQMLLSFNSNTTTAGGAIYVKK 302
Db 61 SFIDNKVTCASSSTTGDMSGGAICAYKTDKVTITGNQMLLSFNSNTTTAGGAIYVKK 120
Qy 303 LELASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPTGTR 362
Db 121 LELASGLTLFNRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTSTTPTGTR 180
Qy 363 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGSTTVDVLKVNTPADSALOYTGNIIFT 422
Db 181 SSIDLGTSAKMTALRSAAAGRAIYFYDPIITGSGSTTVDVLKVNTPADSALOYTGNIIFT 240

XX OS Chlamydomphila pneumoniae.
 XX PN WO9858953-A2.
 XX PD 30-DEC-1998.
 XX PF 19-JUN-1998; 98WO-DK000266.
 XX PR 23-JUN-1997; 97DK-00000744.
 XX PA (BIRK/) BIRKELUND S.
 XX PA (CHRI/) CHRISTIANSEN G.
 XX PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;
 XX DR WPI; 1999-105610/09.
 XX DR N-PSDB; AAX06817.
 XX PT Species-specific test for identifying mammals infected with Chlamydia
 XX PT pneumoniae - comprises detecting antibodies specific for outer membrane
 XX PT proteins of C. pneumoniae or nucleic acids encoding these proteins.
 XX PS Claim 7; Page 43-45; 115pp; English.
 XX CC This polypeptide comprises the novel 97.2 kDa surface exposed protein
 CC Omp5 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
 CC acid sequence was deduced from DNA (see AAX06817) isolated from a C.
 CC pneumoniae expression library. The invention provides 12 novel surface
 CC exposed proteins, Omp4-Omp15 (see AAX06817-28), and nucleic acid
 CC sequences encoding them (see AAX06817-27). A new species specific test is
 CC claimed that is used to identify mammals (including humans) infected with
 CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
 CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used in the
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
 CC proteins can also be used in the immunization of mammals, the nucleic
 CC acids being particularly useful as DNA vaccines for effecting in vivo
 CC expression of antigens. The vaccines may also prevent atherosclerosis and
 CC bronchial asthma, which are possibly associated with C. pneumoniae.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 928 AA;

Query Match 43.1%; Score 2058; DB 2: Length 928;
 Best Local Similarity 46.7%; Pred. No. 3e-127;
 Matches 444; Conservative 142; Mismatches 320; Indels 44; Gaps 20;

QY 1 MKSFPKFPV-STFAIF---PLSMIATETVLDSASPDKNKN-GNFSVRESQBDAGTTL 55
 DB 1 MKSQFSLVLSSTLACFTSCSTVPAATAENIGPDSFGSTNGTTPKNT--TTGIDYT 58

QY 56 FKGNVTLENIPTGTAITKSCFNNTKGDLTFTNGNSLLPQTVDAGTVAGAAVNSVVDK 115
 DB 59 LTGDITLQNL-GDSALTGKCFSDTTSLSFAGKGYSLFSLINIKS-SAEGAAL-SVTTDK 115

QY 116 STTFIGFSSLSFIASPGSSITT--GKGVSCSTGSLSTKNVLSLKNFSTONGAITA 173
 DB 116 NLSLTGFSSLTFLAAPSIVITTSFGKAVKCG-GDITFDNNNGTILPKQDYCEENGAI 174

QY 174 KTLSLGTMTMSALFSENTGS--KKGAIQTSDALITGNQGEVSFSDNTSSDGAIFT 230
 DB 175 KNLNLKNSGTGSIISFEGNKSATCKGGAICATGTVDTNNTAFTLFSNNTAEAGGAINS 234

QY 231 EASVTLSNNAKVSFIDNKVTGASSSTGDMSGGAI CAYKTSTDTKVTLTGNQMLFSNNT 290
 DB 235 TGNCITIGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNQVTFSGNQ 283

QY 291 STTAGGAIYVKKELAS--GGLTLFERNVNGTAPKGGAIATEDSGELSLSDSGDIYF 348
 DB 284 AVANGGAIYAKUTLASGGGGISFNNIVQGTAGNGGAIISLAAGRCLSAERGDITF 343

QY 349 LGNTVITSTTP-GTNRSSIDLGTSAKMTALRSAGRAIFYDYDPTTGSSTTVDLVKNET 407

DB 344 NGNAIVATTQTTKENSIDIGSTAKITNLRAISHSIFFDYDPTITANFAADSTDLNLKA 403
 QY 408 PADSALQYTGNIIFTGKLSETEAAADSKNLTSLKLPVTLGGTSLKHGVTLOTQAFQ 467
 DB 404 DAGNSTDYSGSIVPSGKLSSEDAKADNLSTLTLPVTLTAGNLVLRGVTLDTKGTQ 463
 QY 468 QADSLEMDYGTTLLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLD 526
 DB 464 TAGSSVIMDAGTTLKASTEVEVTLGLSIPVDSLGEKKVWIAAASAKNVALSGPILLD 523
 QY 527 PTGTFYENHSIRNPQSYDILKASGVTSTAVTPDPIMGEKPHYGYGTWGPVW---- 582
 DB 524 NQGNAYENHDLGKTQDFSVQLSALGATTTDVPVATVATPHYGQGTWG-MTWDDT 582
 QY 583 -GTGASTTATFNWTKTYIINPERIGSLVPNSLWNAFIDISSLHYLMETANEGLQGDRA 641
 DB 583 ASTPKTKTATLAWTNTGYLPNPERQGPLVNSLWGSFSDIQAIOGVIERSAITLCSDRGF 642
 QY 642 WCAGLSNFFHKDSTKTRGFRHLGGYVIGNHLTCSDKILSAAFCOLPGRDRDYFAKN 701
 DB 643 WAAGVANFLDKKGEKKRYHKSGGYAIGGAAQTCSSENLSISFAFCOLFGSDKDFLAKN 702
 QY 702 QGTIVYGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLTKY 758
 DB 703 HTDTYAGAFYQH-----ITCSCGFICLLDLKPLQSWSHKPLVLEQLAYSHVSNDLTKY 758
 QY 759 TTYPTVKGWNSDFALEFCGRAPICLDESALFEQYMPFMKLOFVYAHQBFKEQGTGAR 818
 DB 759 TAYPEVKSGWGNFANMNLGASSHSYPEYLHCFDTYAPYIKLNLTYIQDSFSEKGTGR 818
 QY 819 EFGSSRLNLALPIGTRFDKESCDATYNTLGYTVDLVRSNPDCTTTLRISGDSWKT 878
 DB 819 SFDSNLNLSLPIGWKFEKPSDCNDPSYDLTISYVFDLIRNDPKCTTALVIGASWET 878
 QY 879 GTNLARQALVRAGNHFCNFSNFEATSPQSFELRGSRNVDLGAQYQF 928
 DB 879 ANNARQALQVRAGSHYAFSPMEVLFQGFVFEVRGSRINVDLGGKFQF 928

RESULT 6
 ABB90573
 ID ABB90573 standard; protein; 928 AA.
 XX AC ABB90573
 XX DT 29-AUG-2003 (revised)
 XX DT 29-JUL-2002 (first entry)
 XX XX Chlamydia pneumoniae cp0010 protein, SEQ ID NO:95.
 XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029.
 XX Chlamydomphila pneumoniae.
 XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= Signal peptide
 FT 26..928
 FT Protein /note= "Mature protein"
 XX WO200202606-A2.
 XX 10-JAN-2002.
 XX 03-JUL-2001; 2001WO-IB001445.
 XX 03-JUL-2000; 2000GB-00016363.
 XX 11-JUL-2000; 2000GB-00017047.

21-JUL-2000; 2000GB-00017983.
07-AUG-2000; 2000GB-00019368.
18-AUG-2000; 2000GB-00020440.
14-SEP-2000; 2000GB-00022583.
10-NOV-2000; 2000GB-00027549.
22-DEC-2000; 2000GB-00031706.
(CHIR-) CHIRON SPA.
Ratti G, Grandi G;
WPI; 2002-154726/20.
N-PSDB; ABL91231.
Novel Chlamydia pneumoniae protein useful in the manufacture of a
medicament for treatment or prevention of infection due to Chlamydia,
preferably Chlamydia pneumoniae, and for diagnostic purposes.
Claim 1; Page 87-88; 364pp; English.
Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
them. The proteins are predicted to be immunogenic and may therefore be
useful in vaccine production and for diagnostic purposes. Chlamydia
pneumoniae is a common cause of respiratory disease in humans, and is
also involved in the development of cardiovascular diseases such as
atherosclerosis, coronary artery disease, carotid artery stenosis,
myocardial infarction, cerebrovascular disease, aortic aneurysm,
claudication and stroke. The proteins and nucleic acids of the invention
may be used in vaccines and pharmaceutical compositions for the
prevention or treatment of chlamydial infections, particularly Chlamydia
pneumoniae infections. The proteins may also be used in the detection of
Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
DNA probe assay or blotting techniques for determining Chlamydia
pneumoniae gene expression. The present sequence represents a
specifically claimed Chlamydia pneumoniae protein of the invention.
(Updated on 29-AUG-2003 to standardise OS field)

Query Match 42.9%; Score 2048; DB 5; Length 928;
Best Local Similarity 46.5%; Pred. No. 1.4e-126;
Matches 442; Conservative 144; Mismatches 320; Indels 44; Gaps 20;
QY 1 MKSSPPKVPF-STFALF---PLSMIAETVLDSSAGFDGNKN-GNFSVRESQEDAGTYL 55
DB 1 MKSQSWLVSSTLACFTSCSTVFAATAENIGPSDSFDGNTGTTPKNT--TTGIDYT 58
QY 56 FKGNTLENIPGTGTAITKSCFNNTKGLDFTGNGNSLLFQTVDACTVAGAAVNSVVDK 115
DB 59 LTGDTLQNL-GDSAALTGCFSDTTESLSFAGKGYSLFNLKS-SAEGAAL-SVTTOK 115
QY 116 STTFGFSLSPTASPGSITT--GKGVSCSTGSLTKVNSLLSKNFSTUNGAI 173
DB 116 NLSLTGFSLLTFLAAPSIVITPSGKAVKCG--GLTDFDNNGTILPKQDYCEENGAI 174
QY 174 KTLSLGTMTMSALFNSNTSS---KKGAIQTSDALITGNGEVSPSDNTSSDGAIFT 230
DB 175 KNLKNSVCSISFENKNSATKKGAIATCTVITNTTAPLFSNNIAEAGGAINS 234
QY 231 EASVTISNNAKVSFDINKVTGASSSTGDMGSAICAYKTSSTDTKVTLTGNOMLLFSNNT 290
DB 235 TGNCITITGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNSVTFSGNQ 283
QY 291 STTAGGAIYVKLELAS--GGLTFSRNSVNGCTAPKGAIAIEDSCSLSDSGDIVF 348
DB 284 AVANGGAIYAKKTLASGGGVSPFLLTIIVQGTAGNGGAIISLAGECSLSAEGDIYF 343
QY 349 LGNTVTSSTP-GTNRSSIDLTGAKMTALRSAGRAIFYDPITGTSSTVTDVLKVNET 407
DB 344 NGNAIVATTPQTTKNSIDIGSTAKITNLRAISGHSIFFYDPITANTAAOSTDTLNLKA 403
QY 408 PADSALQYTGNIITFTGKLESETEAADSKNLTSKLLQPVTLSSGGLTSLKHGVTLTQTAFTQ 467

DB 404 DAGSTDYSGSIVFSGEKLSDEAKVADNLSTLTKQPVTLTAGNLVLRGVTLDTKGFTQ 463
QY 468 QADSRLEMDVGTITLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGFITLLD 526
DB 464 TAGSSVINDAGTTLKASTEEVTLGLSIPVDSLGEKKVIAAASAKNVALSGPILLD 523
QY 527 PTGTFYENHSRNPQSYDILELKASGTVTSTAVTPDPIMGKFKHYGYGTWGPVW---- 582
DB 524 NQGNAYENHDLGKTQDFSFVQLSALGATTTTDPVAVPTVATPTHYGYGTWGTW-MTWVDDT 582
QY 583 -GTGASTTATFNTKTYIPNPERIGSLVPSNLMNAPIDISSHLVLMETANEGLQDRAF 641
DB 583 ASTPKTKTATLAWTNTGYLPNPEROGPLVPNSLMGSDIQAIOGVIERSAITLCSDRGF 642
QY 642 WCAGLSNFFHKDSTKTRRGFRHLSGGYVIGNHLHTCSDKILSAAPCQLFGRDRDYFAKN 701
DB 643 WAAGVANFLDKDKEKKYRKHSGGYAIGAAQTCSENLSFAFCQLFGSKDFLAKN 702
QY 702 QGTVVGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHTDNDLTKY 758
DB 703 HTDTYAGAFYIQH---ITECSGFICLLDKLPGSWSHKPLVLEGLAYSHVSNLTKY 758
QY 759 TTYPTVKSGWNSDFALBFGGRAPICLDBESALFEQYMPMKIQFVVAHQEGFEQTEAR 818
DB 759 TAYPEVKGSGWNAFNMMLGASSHSYPEYLHCFDTYAPYIKLNTYIRQDSFSEKTEGR 818
QY 819 EFGSRLVNLALPIGIRFEDKESDCQDATYNLTGTVDLVRSNPDCTTTTLRISGDSWTF 878
DB 819 SFDDSNLNLNLSLPIGVKFEKESDCNDFSYDLTSLVVPDLIRNDPKCTTALVISGASWET 878
QY 879 GYNLAROALVLRAGNHCFNSNFEAFSOFELRSGSSNNYVDLGAKYQF 928
DB 879 ANNLAQALQVRAGSHYAFSPMFVLGQFVFEVRGSSRIYNYVDLGKGFQF 928
RESULT 7
ID AAY90237 standard; protein; 928 AA.
AC AAY90237;
XX 12-SEP-2003 (revised)
DT 29-AUG-2000 (first entry)
XX Chlamydia antigen CPN100635.
XX Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
therapy; upper respiratory tract disease; bronchitis; sinusitis;
asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
OS Chlamydia pneumoniae.
XX Key Location/Qualifiers
FH Peptide 1..43
FT Protein /note= "signal peptide"
FT Protein 44..928
FT Protein /note= "mature CPN100635"
XX WO200032794-A2.
XX 08-JUN-2000.
XX 01-DEC-1999; 99WO-CA001147.
XX 01-DEC-1998; 98US-0110339P.
XX 01-DEC-1998; 98US-0110340P.
XX 01-DEC-1998; 98US-0110427P.
XX 01-DEC-1998; 98US-0110428P.
XX 01-DEC-1998; 98US-0110438P.
XX (CONN-) CONNAUGHT LAB LTD.
XX

PI Murdin AD, Oomen RP, Wang J;
 XX WPI; 2000-412339/35.
 DR N-PSDB; AAA30849, AAA30850.
 XX
 PT Nucleic acids encoding polypeptide antigens from Chlamydia useful for
 PT preventing, diagnosing and treating diseases such as community acquired
 PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
 PT asthma.
 XX
 PS Claim 16; Fig 3; 174pp; English.
 XX
 CC This sequence is a Chlamydia antigen of the invention, designated
 CC CPN100635. The nucleic acids (and their complementary sequences) may be
 CC used as diagnostic agents for detecting the presence of nucleic acids
 CC encoding Chlamydia antigens in samples according to standard methods, and
 CC therefore, for diagnosing Chlamydia infections. For example, they may be
 CC used as primers and probes for diagnostic polymerase chain reaction (PCR)
 CC assays. Antisense sequences may be used to down regulate expression of
 CC the proteins and may be used to treat infections. The nucleic acids may
 CC also be used to produce the protein antigens they encode according to
 CC standard recombinant DNA methodologies. The proteins may then be used as
 CC antigens for the production of antibodies (i.e. as vaccines) for
 CC preventing infection by Chlamydia. The antibodies may also be used as
 CC diagnostic reagents for detecting infections. Chlamydia is a pathogen
 CC implicated in the development of (for example) community acquired
 CC pneumonia, upper respiratory tract disease (especially bronchitis and
 CC sinusitis, asthmatic bronchitis, adult-onset asthma and acute
 CC exacerbations of asthma in adults. (Updated on 12-SEP-2003 to standardise
 CC OS field)
 XX
 XX Sequence 928 AA;
 Query Match 42.3%; Score 2021; DB 3; Length 928;
 Best Local Similarity 46.1%; Pred. No. 8.5e-125;
 Matches 438; Conservative 142; Mismatches 326; Indels 44; Gaps 20;
 QY 1 MKSSFPKFPV-STFAIF---PLSMIAETVLDSSASPDGKNK-GNFVSRESQEDAGTTL 55
 DB 1 MKSQFWLVLSTLACFTSCSTVFATAENIGSPDSFGSTNGTYTPKNT--TTGIDYT 58
 QY 56 FKNVILENIPGTGTAITKSCFNNTKGLFTTNGNSLFLQTVTDAGTVAGAAVNSSVVDK 115
 DB 59 LTGDITLQNL-GDAAATKGFCDTTESLSFAGKGYSLSPNKS-SAEGAAL-SVTTDK 115
 QY 116 STTFIGFSSLSPTASPGSSITT--GKAVSCSTGSLSLTKVNSLLRSKNFSTNGAITA 173
 DB 116 NLSLTGFSLLFLAAPSIVITPSPGKAVKCG-GDITFDNNGTILPKQDYCEENGGAIST 174
 QY 174 KTLSLGTGTTMSALFSENTSS--KKGAIQTSDALITITGNGEVSFSDNTSSDGGAAIFT 230
 DB 175 KNLSLKNSTGISFEGNKSSATKGAICATGTVDTTNTATPLFSNNIAEAGGAINS 234
 QY 231 EASVTISNNAKVSFINKVTGASSSTGDMGGAICAYKTSTDKTVTLTGQMLFLSNNT 290
 DB 235 TGNCITITGNTSLVFSNSVT---ATAG--NGCAL-----SGDADVTISGNQSVTFSGNQ 283
 QY 291 SITAGCAIYVKKLELAS--GGLTLFRNSVNGCTAPKGAIAIEDSGELSLSDSGDIYF 348
 DB 284 AVANGAIIYAKKLTLASGGGGNPNNNIVQGTAGNGGAISILAAGECSLFSAGDHYL 343
 QY 349 LGNTVSTTP-GTNRSSIDLTSAKMTALRSAGRAIYFVDPIITGSSVTVDVLKNET 407
 DB 344 NGNAIVATTPTQTKRNSIDIGSTGKHDLRAISGHSIFFDYDPTANTADSTDTLNKA 403
 QY 408 PADSALOYTGNIIPTGEKLSSEEAASKNLTKLQPVTLSGTSLKHGVTILQOAFQ 467
 DB 404 DAGNSTDYSGSIVFSGEKLSEDEAKVADNLTSLKQPVTLTAGNLVLRGVTLDTKGFTQ 463
 QY 468 QADSRLMDVGTLEPA-DTSINNLVINLSSIDGAKKAKIETKATSKNLTLSGTTLLD 526
 DB 464 TAGSSVMDAGTTLKASTBEVLTGLSIPVDSLGEKGKVVIAASAASKNVALSGPILLD 523

QY 527 PTGTFFYENHSLRNPSQSYDILELKASCTVTSTAVTPDPTMGKEKPHYGYQGTWGPVW---- 582
 DB 524 NQGNAYENHDLGKTQDFSFQLSALGTATTDDVPAVPTVATPTTHYGYQGTW-MTWVDDT 582
 QY 583 -GTGASTATTAFTNWTGTVIPNPERIGSLVPSNLWNAFIDISSLHVLMTANEGLOGDEAF 641
 DB 583 ASTPKTATLAWNTGYLNPFRQGPLVPSNLWGSFSDIQAIQGVIERISALTLCSDRGF 642
 QY 642 WCAGLSNFFHKOSTKTRGRFRLHSGGYVIGGNLHSCDKILSAAFCQLFGRDRDYFVAKN 701
 DB 643 WAAGVANFLDKKKGKKRYKHKSGGYAIGGAACTCSENLSFAFCQLFGSDKDFLAKN 702
 QY 702 QGTVYGCTLYXONNETYISLPCKLRPCSLVSP---TEIPVLFSGNLSYHTDNDLTKTY 758
 DB 703 HTDTYAGAFYIQH-----ITCSPGFIGCLLDKLPQSWSHKPLVLEGOLAYSHVSNDLTKTY 758
 QY 759 TTYPTVKGSGNDSFALEFGGRAPICLDESALFQYMPFMKLFQVYAHQEGKEQGTAR 818
 DB 759 TAYFEVKGSGNNAFNNMLGASSHSYPEYLHCFTYAPYIKNLITYIQDSFSKGTGR 818
 QY 819 EFGSSRLVNLALPIGRFDPKESQCDATYNTLTGYTVDLVRSNPDCTTTLRISGDSWKT 878
 DB 819 SFDDSNLFNLSPGVKFEKFCNDPFSYDLTILSYVPDLIRNDPKCTTALVISGASWET 878
 QY 879 GTNLQAQVLIRAGNHCFNSNFEAFSOPFELRGSSRNYNVDLGAKYQF 928
 DB 879 ANNLAQALQVRAGSHYAFSPMEVLGQFVFEVRGSSRIYNVDLGGKQF 928
 RESULT 8
 AAY69369
 ID AAY69369 standard; protein; 918 AA.
 XX
 AC AAY69369;
 XX
 DT 12-SEP-2003 (revised)
 DT 19-JUN-2000 (first entry)
 XX
 XX Amino acid sequence of the CPN100395 polypeptide.
 XX CPN100395; Chlamydia infection; immune response; vaccine.
 XX Chlamydia pneumoniae.
 XX WO200011183-A2.
 XX 02-MAR-2000.
 XX
 XX 18-AUG-1999; 99WO-IB001449.
 XX 20-AUG-1998; 98US-0097187P.
 XX 20-AUG-1998; 98US-0097188P.
 XX 20-AUG-1998; 98US-0097189P.
 XX 20-AUG-1998; 98US-0097190P.
 XX 20-AUG-1998; 98US-0097195P.
 XX 20-AUG-1998; 98US-0097196P.
 XX 20-AUG-1998; 98US-0097197P.
 XX 27-AUG-1998; 98US-0097191P.
 XX 17-AUG-1999; 99US-00376770.
 XX (CONN-) CONNAUGHT LAB LTD.
 XX Murdin AD, Oomen RP;
 XX WPI; 2000-224703/19.
 XX N-PSDB; AA261509.
 XX
 PT Novel antigens and corresponding DNA molecules that can be used to
 PT prevent, treat and diagnose disease caused by Chlamydia infection in
 XX mammals, especially humans.
 PS Claim 19; Fig 15-E; 201pp; English.

CC AAY69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides
 CC are present in the bacterial membrane structure, in the external vicinity
 CC of the membrane structure, in the inclusion membrane structure, in the
 CC external vicinity of the inclusion membrane structure, and in the
 CC cytoplasm of the infected cell. The polypeptides may be used to prevent,
 CC treat and detect the presence of Chlamydia infection and/or the presence
 CC of Chlamydia in a sample. The polypeptides may also be used to induce an
 CC immune response in a mammal. The vaccine vector comprising the
 CC polynucleotides is used to induce an immune response in a mammal.
 CC Antibodies directed against the polypeptides may also be used
 CC therapeutically to treat and/or prevent a Chlamydia infection. (Updated
 CC on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 918 AA;

Query Match 42.0%; Score 2006; DB 3; Length 918;
 Best Local Similarity 45.6%; Pred. No. 8.3e-124;
 Matches 432; Conservative 150; Mismatches 316; Indels 50; Gaps 20;

QY 1 MKSFPKVFSTFAIFPLSMI-----ATETVLDSSAFDGN-KNGNFSVRESQEDA-GTTY 54
 Db 1 MRSSFLLISSLAPFLMVSADAADLTGSRDSYNGDTSTTEFTPKAATSDAGTTY 60
 QY 55 LFKGNVTLEIPGTGTAITKSCFNNTKGLDPTGNGSLLPOTVDAGTVAGAAVNSVVD 114
 Db 61 ILGDVSIQ-AGKQTSLTSCFSNTAGNLTGNGFSLHFDNIISSTVAGVYVNSTAAS 119
 QY 115 KSTTIGRSSLSFIAPSGSIITGKAVSCSGSLTKNVSLFKNPSTDNGAITAK 174
 Db 120 GITKFSGFSTLMLAAPR---FTGGAIKITDG-LVFESIGNLDJNENASNGGAINTK 175
 QY 175 TLSLTGTTMSALFSENTSKGGAITQTSALITGNGQEVSFSDNTSDSGAAIFEASV 234
 Db 176 TLSLTGTFEFAVLGNSSQOGAIVASGDSVISENAGILSFGNSSATTSGCAISAGNL 235
 QY 235 TISNNAKVSFIDNKVTGASSTTGDMSGGAI CAYK--TSTDVKVLTGQMILLFSNNTST 292
 Db 236 VISNNQNIFFDGCAT-----TNGGAIDCNKAGANPDPILTLSGNESHFLNNTAG 286
 QY 293 TAGGAIYVKLELAG-GLTFRSNVNGGTAPKGAIAIEDSGELSLSDGDIVFLGN 351
 Db 287 NSGGAIYTKGVLSGGRGVLFNNKAANAT-PKGAIAIILDSGEISISADLGNIIIFGN 345
 QY 352 TWTSTT---PGNRRSIDLGTSAKMTALRSAGRAIFYDPITTGSTTTTVDLVKNETP 408
 Db 346 T-TSITGSPASVTRNAIDLASNAKFLNLAATRGKVI FYDPIT---SSGATDKLSNKAD 401
 QY 409 ADSALQYTNIIPTGKLGSETEAADSKNLTSKLLQPVTLSSGTLSLKHGVTLOTQFTQ 468
 Db 402 AGSGNTYEGYIVFSGEKLSEELKPDNLKSTFTQAVELAAGALVLKDGVTVVANITQV 461
 QY 469 ADSLEMDVGTTLLE-PADTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLDP 527
 Db 462 EGSKVMDGTTPEAGAEVTLNGLAINDSLDGTWKAIKATAASKDVALSPIMLVDA 521
 QY 528 TGTFFYHSLRNQPSQDILLELKASGTVTSTAVTPDPMCKEPHYGQGTWPIW---GT 594
 Db 522 QGNYEHNLSQOQVFLIELSAQGTWTTTIDIPTELTNTNHYGQGNWN-LVWVDDAT 580
 QY 585 GASTTATFNWTKYTPNPERIGSLVPNSLWNAFIDISLHYLMETANEGLQGDRAFWCA 644
 Db 581 AKTKNATLAWTKYKPNRQGPLVPSLWGSFVDVRSIQSLMDRSTSLSSSTNLWVS 640
 QY 645 GLSNFPHKSTKTRGRPHSLGGVIGGVLGNLHSCDKLSAFCQLFDRDRDYFAVKNQGT 704
 Db 641 GIADFLHEDQGNQSVRHSAGVALGCGGFTASENFNFACQLFCYDKDLVKNHHT 700
 QY 705 VYGGTLYYQH---NETYISLPCKLRPCSLSYVPTETPVLPSGMLSYTHTDNDLTKYTTY 761
 Db 701 VYAGMSYRHLGESKTLAKI-----LSGNSDSLFPFVENARFAYGHTDNNMTTKYTY 752
 QY 762 PTVKGSGNDSFALEFGGRAPICLD-ESALFEQYMPKMLQFYVYHQEGKEQGTAREF 820

Db 753 SPVKGSGNDAGFIECGGAIPVVASGRRSWVDTHTPFLNLEMIYAHQNDFKENGTEGRSF 812
 QY 821 GSSSLVNLALPIGIRPKESDCQDATNLTILGYTVDLVRSNPDCTTTLRISGDSWKTRGT 880
 Db 813 QSEDLFNLAIVGKIKFEKFS--KSTYDLSIAYVPDVRNDPGCTTTLMVSGDSWSTCGT 870
 QY 881 NLARQALVLRAGNFCNSNFEAFSQSFELGRSSRNYNVDLGAKYQF 928
 Db 871 SLRQALLVRAGNHAFASNFVFSQFEVELGRSSRYAIDLGGRF 918

RESULT 9

AAW88422
 ID AAW88422 standard; protein; 918 AA.

XX AAW88422;

DT 17-OCT-2003 (revised)

DT 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp9.

XX Omp9; outer membrane protein 9; surface exposed protein; antigen;
 KW infection; diagnosis; vaccine; atherosclerosis; asthma.

XX Chlamydophila pneumoniae.

XX WO9858953-A2.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-DK000266.

XX 23-JUN-1997; 97DK-00000744.

XX (BIRK/) BIRKELUND S.

XX (CHR/) CHRISTIANSEN G.

PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

XX WPI; 1999-105610/09.

DR N-PSDB; AAX06821.

XX Species-specific test for identifying mammals infected with Chlamydia
 pneumoniae - comprises detecting antibodies specific for outer membrane
 proteins of C. pneumoniae or nucleic acids encoding these proteins.

XX Claim 7; Page 56-58; 115pp; English.

PS This polypeptide comprises the novel 96.7 kDa surface exposed protein
 XX Omp9 of the human respiratory pathogen Chlamydia pneumoniae. Its amino
 CC acid sequence was deduced from DNA (see AAX06821) isolated from a C.
 CC pneumoniae expression library. The invention provides 12 novel surface
 CC exposed proteins, Omp4-Omp15 (see AAX068417-28), and nucleic acid
 CC sequences encoding them (see AAX06816-27). A new species specific test is
 CC claimed that is used to identify mammals (including humans) infected with
 CC Chlamydia pneumoniae. The test comprises detecting antibodies specific
 CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used in the
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and
 CC proteins can also be used in the immunization of mammals, the nucleic
 CC acids being particularly useful as DNA vaccines for effecting in vivo
 CC expression of antigens. The vaccines may also prevent atherosclerosis and
 CC bronchial asthma, which are possibly associated with C. pneumoniae.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 918 AA;

Query Match 41.9%; Score 2001; DB 2; Length 918;

Best Local Similarity 45.4%; Pred. No. 1.8e-123;

Matches 433; Conservative 151; Mismatches 309; Indels 60; Gaps 21;

QY 1 MKSFPKVFSTFAIFPLSMI-----ATETVLDSSAFDGN-KNGNFSVRESQEDA-GTTY 54

PI Murdin AD, Oomen RP, Wang J;
XX WPI; 2000-412339/35.
DR N-PSDB; AAA30849, AAA30850.
DR
XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT preventing, diagnosing and treating diseases such as community acquired
PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT asthma.
XX
PS Claim 16; Fig 3; 17app; English.
XX
CC This sequence is a Chlamydia antigen of the invention, designated
CC CPN100635. The nucleic acids (and their complementary sequences) may be
CC used as diagnostic agents for detecting the presence of nucleic acids
CC encoding Chlamydia antigens in samples according to standard methods, and
CC therefore, for diagnosing Chlamydia infections. For example, they may be
CC used as primers and probes for diagnostic polymerase chain reaction (PCR)
CC assays. Antisense sequences may be used to down regulate expression of
CC the proteins and may be used to treat infections. The nucleic acids may
CC also be used to produce the protein antigens they encode according to
CC standard recombinant DNA methodologies. The proteins may then be used as
CC antigens for the production of antibodies (i.e. as vaccines) for
CC preventing infection by Chlamydia. The antibodies may also be used as
CC diagnostic reagents for detecting infections. Chlamydia is a pathogen
CC implicated in the development of (for example) community acquired
CC pneumonia, upper respiratory tract disease (especially bronchitis and
CC sinusitis, asthmatic bronchitis, adult-onset asthma and acute
CC exacerbations of asthma in adults. (Updated on 12-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 885 AA;
Query Match 41.6%; Score 1987.5; DB 3; Length 885;
Best Local Similarity 46.9%; Pred. No. 1.3e-122;
Matches 420; Conservative 136; Mismatches 302; Indels 37; Gaps 16;
QY 51 GTTYLFGKGVNLENTPGTGTALTGKCFNNTKGDLFTGNGNSLLPQTVDAAGTVAGAAVNS 110
DB 11 GIDYTLTGDTLQNL-GDAAALTGKCFDSTSLSPAGKGYSLSFNLIK-S-BAEGAL-S 67
QY 111 SVVDKSTTFIFGFSLSFIASPGSSIT--GKGAIVCSSTGSLTKVSLFKNFSTDNG 168
DB 68 VTDDKNLSLTGFSLLTFLAAPSIVTPSGKAVKCG-GDLTFDNNGTILFKQDYCEENG 126
QY 169 GAITAKTSLTGTMTSALESENTSS---KKGAIQTSALTITGNGOGEVSFSDNTSSDSG 225
DB 127 GALTSTKLSLKNSTGSGISFEGNKSSATGKGAICATGTVDTITNTAPTILFSNNIAEAG 186
QY 226 AAIPTASVTISNNAKVFDIDNKVTCASSSTTGDMSGGAICAYKTSTDTKVTLTGNQMLL 285
DB 187 GAINSTGNCITITGNTSLVFSNSVT---ATAG--NGGAL-----SGDADVTISGNSQSVT 235
QY 286 FSNNTSTTAGGAIYVKKLELAS--GGTLTFSRNVNGTAPKGAJAIEDSGELSLSADS 343
DB 236 FSGNQAVANGGAIYAKKILASGGGGNPFNNIVQGTAGNGAISILAAEGCSLPSEA 295
QY 344 GDIVFLGNTVTSTTP-GTNRSSIDLTSKAMTALRSAGRAIYFYDPIITGSSSTVTDVL 402
DB 296 GDHYLNGNAIVATTPQTTKNSIDIGSTGKDHLEIRAISSHSIFPYDPIITANTADSDTTL 355
QY 403 KVNETPADSALQVTGNIITFGEKLSATEAADSNNLTSKLLQPVTLTSGTTLSLKHGVTLOT 462
DB 356 NLNKADAGNSTDYSGSIVFSGEKLSEDEAKVADNLNLSLTQPVTLTLAGNLVLRKGVTLDT 415
QY 463 QAPTQQADSRLEMDVGTTLLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGT 521
DB 416 KGFTQTAGSVIMDAGTTLKASTEEVTLTGLSIPVDSLGEKGVVIAAASAASKNVALSGP 475
QY 522 ITLLDPTGTTFYENHSLRNPOSYDILELKASGTVTSTATPDPIMGEKPHYGQGTWGPV 581
DB 476 ILLLDNQNAYENHDLGKTQDFSFVQLSALGTATTTDVPVATPTVATPHYGQGTWGW-MT 534

QY 349 LGNTVTSTTP-GTVRRSSIDLTSKAMTALRSAGRAIYFYDPIITGSSSTVTDVLKVNET 407
DB 344 NGAIVATTPQTTRKNSIDIGSTAKITNLRAISHSIFFYDPIITANTAASTDITLNLKA 403
QY 408 PADSALOYTGNIIFTGEKLSATEAADSNNLTSKLLQPVTLTSGGTLSLKHGVTLOTQFTQ 467
DB 404 DAGNSTDYSGSIVFSGEKLSEDEAKVADNLNLSLTQPVTLTLAGNLVLRKGVTLDTKGTQ 463
QY 468 QADSRLEMDVGTTLLEPA-DTSTINNLVINISSIDGAKKAKIETKATSKNLTLSGTITLLD 526
DB 464 TAGSVIMDAGTTLKASTEEVTLTGLSIPVDSLGEKGVVIAAASAASKNVALSGPILLD 523
QY 527 PTGTFYENHSLRNPOSYDILELKASGTVTSTATPDPIMGEKPHYGQGTWGPVW---- 582
DB 524 NQGNAYENHDLGKTQDFSFVQLSALGTATTTDVPVATPTVATPHYGQGTWGW-MWVDDT 582
QY 593 -GTGASTTATFNWTKTIGYIPNPERIGSLVPSNLMNAFIDISLHYIMETANEGLQDRAP 641
DB 593 ASTPKTKATLAWTNGYLPNPGROGPLVPSNLMSGFSDIQAIQGVIERALSALTLCSDRGF 642
QY 642 WCAGLSNFHKDSTKTRGFRHLSCGYVIGMHLTCSKILSAARCOLFGRDRDYFVAKN 701
DB 643 WAAGVANFLDKDKGKERYKHKSGYAIAGAAQTCSENLTSPAPCOLFGSKDFLVAKN 702
QY 702 QGTVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPVLFGNLSYTHTDNDLTKYK 758
DB 703 HTDTYAGAFYIQH----ITECSGFTGCLLDKLPKGSWSHKPLVLEQGLAYSHVNDLKYK 758
QY 759 TTYPTVKGSGWNSDALEFGGRAPICLDESALFEQYMPFMKLFQVYAHQEGFKQGTEAR 818
DB 759 TAYPEVKGSGWNAFNMMLGASHSYPEYLHCFDVIAPYIKLNTLYIRQDSFSEKTEGR 818
QY 819 EFGSRLVNLALPIGIRFPKESDQDQATNLTGYTVDLVRNPDCTTILRISGDSWKT 878
DB 819 SFDDSNLFLSLPIGVKFEKFSKDNDFSYDLTSLYVPDLIRNDPKCTTALVSGASWETY 878
QY 879 GTNLAQALVLRAGNHCFSNPFARSOPSEELRGS 914
DB 879 ANNLAQALQVRAGSHYAFSPMEVLGQFVFEVRGS 914
RESULT 11
AAI90238
ID AAY90238 standard; protein; 885 AA.
AC
XX
XX
DT 12-SEP-2003 (revised)
DT 29-AUG-2000 (first entry)
DE
XX Mature Chlamydia antigen CPN100635.
XX Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
XX therapy; upper respiratory tract disease; bronchitis; sinusitis;
XX asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
XX Chlamydomphila pneumoniae.
OS
XX WO200032794-A2.
XX
XX 08-JUN-2000.
XX
XX 01-DEC-1999; 99WO-CA001147.
XX
XX 01-DEC-1998; 98US-0110339P.
XX 01-DEC-1998; 98US-0110340P.
XX 01-DEC-1998; 98US-0110427P.
XX 01-DEC-1998; 98US-0110428P.
XX 01-DEC-1998; 98US-0110438P.
XX
XX (CONN-) CONNAUGHT LAB LTD.

QY 879 GTNLARQALVLRAGNHCFFNSNPAFQSPFELRGSSRNYNVDLGAKYQF 928
 DB 879 GTNLSRQAGIGRAGIFAFSPNLEVTNLSNMEIRGSSRSYNADLGKRFQF 928

RESULT 13
 ID ABB90542
 ID ABB90542 standard; protein; 928 AA.

XX ABB90542;
 DT 29-AUG-2003 (revised)
 DT 29-JUL-2002 (first entry)
 XX Chlamydia pneumoniae cp6731 protein, SEQ ID NO:33.

XX Chlamydia pneumoniae cp6731 protein, SEQ ID NO:33.
 KW Chlamydia infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029.

XX Chlamydia pneumoniae.

XX Key Location/Qualifiers
 FH 1..26
 FT Peptide /label= Signal_peptide
 FT Protein 27..928
 FT /note= "Mature protein"

XX WO200202606-A2.

XX 10-JAN-2002.

XX 03-JUL-2001; 2001WO-JB001445.

XX 03-JUL-2000; 2000GB-00016363.

XX 11-JUL-2000; 2000GB-00017047.

XX 21-JUL-2000; 2000GB-00017983.

XX 07-AUG-2000; 2000GB-00019368.

XX 18-AUG-2000; 2000GB-00020440.

XX 14-SEP-2000; 2000GB-00022583.

XX 10-NOV-2000; 2000GB-00027549.

XX 22-DEC-2000; 2000GB-00031706.

XX (CHIR-) CHIRON SPA.

XX Ratti G, Grandi G;

XX WPI; 2002-154726/20.

XX N-PSDB; ABL91200.

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.

XX Claim 1; Page 57; 364pp; English.

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a

CC specifically claimed Chlamydia pneumoniae protein of the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 928 AA;

Query Match 41.5%; Score 1982; DB 5; Length 928;
 Best Local Similarity 45.2%; Pred. No. 3.3e-122;
 Matches 429; Conservative 150; Mismatches 327; Indels 44; Gaps 19;

QY 1 MKSSFPKVFSTFAIFPLSM-----TATEVLSSASFDGNKGNFVSRESQEDA-GTT 53
 DB 1 MKSSLHFLISSSLALPLSLNFSAFAAIVEINLGTNFSFG--PGTYTPPAQTINADGTI 58
 QY 54 YLFKGNVTLENIPTGTATITKSCNNTKGDITFTCGNSLLFTQVDAGTVAGAAVNSVV 113
 DB 59 YNLTDVSIITN-AGSPALTATACPKETTCNLSFGHGYQFLQNDIAG--ANCTTTAA 115
 QY 114 DKSTTFIFGSSIFASPGSSITTTGKAVSCSTGSLTKNVSLLFKNFSTDNCGAITA 173
 DB 116 NKLSFSGFSYLSLIQT--TWATGTGAIK-STGACSIQSNVSCYFGQNFSDNGGALQG 172
 QY 174 KTLSTGTMTGALFSENSTSKKGGAIQTSDALTTTGNQGEVSFSDNTSSDGAALFTEAS 233
 DB 173 SSISLS-LNPNLTFAKNKATQGGALYSTGGITINNTLNSASFSENAAANGGALYTEAS 231
 QY 234 VTISNAKVSPIDNKVTGASSTTTCGMSGGAIKAYKSTDTKV-TLTGNMLLESNTST 292
 DB 232 SFISSNKAISPTNNSVTATSA-----TGGALYCSSTAPKPVLTLSNGELNFGNTAI 285
 QY 293 TAGGAIYVKLELASGGLTFLFRNSVNGGTAPKGAIAIEDSGELSLSDSGDIVFLNGT 352
 DB 286 TSGGAIYTDNLVLSGGPTLFKNNSAIDTAAPLGGAIADSGSLSLSGDITPEGNT 345
 QY 353 V---TSTTPGTRNSIDLG-TSAKMTALRSAGRAIYFYDPIITGSSSTTVTLVKNETP 408
 DB 346 VVGKASSQTTRNSINIGNTNAKIVLRASQNTIIFYDPIITTSITTAALSALNAGPD 405
 QY 409 ADSALQYTGNIIFTGEKLTSEAAADSKNLTSLKLPVTLGGTSLKHGVTLQTOAFTQ 468
 DB 406 LAGNPAYQGTIVFSGEKJSEAAEADNLKSTIQPFLTAGQLSLKSGVTLVAKSFSQS 465
 QY 469 ADSRLMDVGTTLLEPADTSTINNLVINISSIDGAKAKIETKATSKNLTSGTITLLDPT 528
 DB 466 PGSTLLMDAGTTLETADGITINNLVNLVDSLKXETKATLKAQASQVTLTSGSLSDVPS 525
 QY 529 GTFYENHSLRNPQSYDILELKAS--GTVTSTAVTPDPIMGEKPHYGYOGTWGPIVWGTGA 586
 DB 526 GNVYEDVSWNPQVFSCLTLDADPANIHITDLADPLEKNPIHWGYQGNWA-LSWQEDT 584
 QY 587 ST---TATFNWTKGYIPNPERIGSLVPSNLNNAFIDISLHYLMETANEGLQDRAFWC 643
 DB 585 ATKSKAATLTWTGTGYNPNPERRGTULVANTLWGSFVDVRSIQQLVATKVRQSDTRGIWC 644
 QY 644 AGLSNFFHKDSTKTRRGFRHLGGYVIGGNLHTCSDKILSAAFCQLFGRDRDYFAKNQG 703
 DB 645 EGLSNFFHKDSTKINKGFRHISAGYVVGATTTILASDNLITAAFCQLFGKDRDHFINKRA 704
 QY 704 TVYGGTLYYQHNETYISLPCKLRPCSLSYVP---TEIPULFSGNLSYTHTDNLDKITYTT 760
 DB 705 SAYAASLHLQHLATLSS-----PSLLRYLPGESEQPVLFDAQISYIYSKNTMKTYTQ 758
 QY 761 YPTVKSGWNGDSFALFEGGRAP-ICIDESALPEQYMPFMKLOFYAHOEKGKQGTG-AR 818
 DB 759 APKGESWYNDGCALAEALASSLPHALTALSHGELFYAYFPFIKVEASYIHQDSFKERNITLVR 818
 QY 819 EFGSSRLVNLALPIGIRFDKESCDQATNLTLYTVDLVRNPDCTTTLIRISGDSWKTF 878
 DB 819 SFPSDGLINVSPIGITTFERSNERASYEATVIYVADVYRKNPDCCTALLINNTSKTT 878
 QY 879 GTNLARQALVLRAGNHCFFNSNPAFQSPFELRGSSRNYNVDLGAKYQF 928
 DB 879 GTNLSRQAGIGRAGIFAFSPNLEVTNLSNMEIRGSSRSYNADLGKRFQF 928

KW vaccine; antibacterial; community acquired pneumonia; bronchitis;
 KW sinusitis; acute respiratory disease; upper respiratory tract disease;
 KW asthma; atherosclerosis.

XX Chlamydophila pneumoniae.

XX Key Location/Qualifiers
 FH Peptide /label= Signal_peptide
 FT Protein 12..936
 FT /label= 98_kDa_membrane_protein
 XX

PN WO200032784-A1.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-CA001148.

XX 01-DEC-1998; 98US-0110439P.

PR 03-MAY-1999; 99US-0132272P.

XX (CONN-) CONNAUGHT LAB LTD.

XX Murdin AD, Oomen RP, Wang J, Dunn P;

XX WPI; 2000-412330/35.

DR N-PSDB; AAA48838, AAA48839.

XX New polynucleotide encoding the Chlamydia 98 kilodalton outer membrane
 PT protein, useful for preventing or treating Chlamydia infection.

XX Claim 16; Fig 1; 98pp; English.

XX The present sequence is CPN100640, the 98 kDa outer membrane protein from
 CC Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of community
 CC acquired pneumonia and upper respiratory tract symptoms and diseases,
 CC including bronchitis and sinusitis. It also has an association with
 CC atherosclerosis and asthma. The 98 kDa outer membrane protein is a C.
 CC pneumoniae-specific antigen which can confer immune protection against
 CC Chlamydia infection. The nucleotide sequence encoding the protein or the
 CC protein itself may be administered as a vaccine to prevent or treat
 CC infection and they may also be used to diagnose infection. The gene
 CC encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA by
 CC PCR. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 936 AA;

Query Match 41.2%; Score 1965; DB 3; Length 936;

Best Local Similarity 43.4%; Pred. No. 4.4e-121;

Matches 411; Conservative 179; Mismatches 327; Indels 30; Gaps 16;

QY 1 MKSSPFKVFSTFAIF-PLSMINATEVLDSS-ASFDGKNGNFSVRESOE-DAGTTLFK 57
 DB 1 MKSSVSWLFFSSIPFSSLSIVAARVTLDSNNNSYDGSNGTTFVFTTDAAGTYSLL 60
 QY 58 GNVLTENIPGTGTAITKCFNNTKGDLTFTGNGSNLLFOTVDAGTVAGAAVNSVVDKST 117
 DB 61 SDVSPQAGALGIPLASGCFLEAGDLTFQGNHALKFAFINAGSSAGTVASTAADKNL 120
 QY 118 TFIGFSLSPFASPGSSIT-TGKAVSCSTGSLSLTKNVSLLFSKNPSTDNCGAITAKTL 176
 DB 121 LFNDPSRLSIISCPILLSPTGCALK-SVGNLSLTGNSQIIETQNFSSDNGGVINTKNF 179
 QY 177 SLTGTTMSALFSENT--SSKKGAIQTSDALITTCNGEVSFSDNTSSDSGAALFTEASV 234
 DB 180 LLSGTSQFASFRNQAFPTGQGVVATGTTITENSPGIVSFQNLAKGGGALYSIDNC 239
 QY 235 TISNAKVSFDKNKVTGASSSTTGDMSGGAICAYKSTDTKVTLTGNQMLLFSNNTSTA 294
 DB 240 SITDNFQVIFDGNSAWEAQA-----QGAICCC--TTTDKTVTLTGNKLSFTNNTALTY 292
 QY 295 GGAIYVKKLEIASGGLTIFSRNSVNGGTAPK--GGAIAIEDSGELSLSDSGDIVFLGNT 352

Db 293 GGATSGLKVSISAGGPTLFQSN-ISGSSAGGGGGAINIASAGELALSATSQDITFNNNQ 351
 QY 353 VTSTTPGTNRSSIDLGTSAKMTALRSAGRAIYFYDPTTGSSTVTVDLVKVNTPADSA 412
 Db 352 VTNGSTST-RNAINI IDTAKVTSIRAATGOSIYFVDPITNPGTAASTDTLNLADANSE 410
 QY 413 LOYTGNIIFPGEKLSSETAADSKNLTKLLOPVTLSGGTSLKHGVTLOTQAFQQAQDSR 472
 Db 411 IEYGGAIVFSGEKLSPEKAIKAAAVTSTIROPVLAARGDLVLRDGVTVTFKDLTQSPGR 470
 QY 473 LEMDVGTTLEPADTS-TINNIVINISSIDGAKKAKIETKATSKNLTLSGTTLLDPTGTF 531
 Db 471 ILMOGTTLTSAKEANLSLNGLAVALNLSLDGTNKAAKTEAADKNLSLSTIALIDTEGSP 530
 QY 532 YENHSLRNPOSYDILELK---ASGTVTSTAVTPPIMGEKPHYGQGTWGIWGTGAST 588
 Db 531 YENHLSKASTYPLLELTTAGANGTITLQALSTLTLPETHYGYQGNW-QLSWANATSS 589
 QY 589 -TATFNWTKGYIINPERIGSLVPSNLWNAIDIDISSLHYLMETANEGLQGDRAFCAGLS 647
 Db 590 KIGSINWTRTGYIPSPERKSNLPLNSLWGNFIDIRSINQLIETKSSGGEFFERELWLGIA 649
 QY 648 NFEHKDSTKTRRGPRHLSGGYVIGGNLHTCSDKILSAAFCQLFGDRDRDYFVAKNQGTVYG 707
 Db 650 MFFRDSMPTRHGFPHISGGYALGITATTPAEDQLTFAFCQLFARDRNHITGKNHGDYTG 709
 QY 708 GTLYYQHNETYISLPCKL-----RPSLSVVPTEIPVLFSGNLSYTHTDNDLTKYTTY 761
 Db 710 ASLYPHHTTEGLFDIANFLWKGATRAPVWLSEISQIPLSFDAKFSYLTHTDNHMKTYTDN 769
 QY 762 PTVKSGWNSDPALEFFGGRAPICLDESALFEQYMPFMKLQFYVAHOEGFKEQGTAREFG 821
 Db 770 STIKSGWENDAFCADLGASLPFVISVPYLLKEVEFPVKQYIYAHQQDFYERHAEGRAN 829
 QY 822 SSRLVNLALPIGIRFDKESDCODATYNTLTGYTVDLVRSPDCTTTLRISGDSWKTFTGN 881
 Db 830 KEELINVELPIGVTERDSKSEKGYDLTLMVILDAYRNPCKQTSLIASDANMMAYGTN 889
 QY 882 LARQALVLRAGNHFCFNSNFEAFSFPFELRGSSRNYNVDLAKYQF 928
 Db 890 LARQGSFVRAAHNFQVNPHEIFGQFAFEVRSRRNNTNLGSKFCF 936

Search completed: August 10, 2004, 13:12:55

Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 13:11:51 ; Search time 23 Seconds
(without alignments)
2082.996 Million cell updates/sec

Title: US-09-428-122-2
Perfect score: 4774
Sequence: 1 MKSSFPKFVFSTFAIFLSM.....FELGSSRNYNVDLGAKYQF 928

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :
1: /cgn2/6/ptodata/2/iaa/5A COMB pep.*
2: /cgn2/6/ptodata/2/iaa/5B COMB pep.*
3: /cgn2/6/ptodata/2/iaa/6A COMB pep.*
4: /cgn2/6/ptodata/2/iaa/6B COMB pep.*
5: /cgn2/6/ptodata/2/iaa/PTUS COMB pep.*
6: /cgn2/6/ptodata/2/iaa/backfiles1 pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	2802.5	58.7	597	4	US-09-198-452A-29	Sequence 29, Appl
2	1940	40.6	930	4	US-09-198-452A-470	Sequence 470, App
3	1917.5	40.2	927	4	US-09-198-452A-472	Sequence 472, App
4	1856	38.9	949	4	US-09-198-452A-478	Sequence 478, App
5	1572.5	32.9	943	4	US-09-198-452A-474	Sequence 474, App
6	1417.5	29.7	922	4	US-09-198-452A-15	Sequence 15, Appl
7	1377.5	28.9	973	4	US-09-430-723-2	Sequence 2, Appl
8	1259	26.4	671	4	US-09-198-452A-468	Sequence 468, App
9	1214	25.4	230	4	US-09-198-452A-30	Sequence 30, Appl
10	1203.5	25.2	507	4	US-09-198-452A-32	Sequence 32, Appl
11	1130	23.7	1132	4	US-09-198-452A-466	Sequence 466, App
12	1128	23.6	1012	4	US-09-612-402B-2	Sequence 2, Appl
13	1126.5	23.6	1006	4	US-09-556-877-190	Sequence 190, App
14	1126.5	23.6	1006	4	US-09-620-412C-190	Sequence 190, App
15	1126.5	23.6	1006	4	US-09-598-419-190	Sequence 190, App
16	1124.5	23.6	982	4	US-09-556-877-176	Sequence 176, App
17	1124.5	23.6	982	4	US-09-620-412C-176	Sequence 176, App
18	1124.5	23.6	982	4	US-09-598-419-176	Sequence 176, App
19	1117.5	23.4	984	4	US-09-612-402B-43	Sequence 43, Appl
20	1110.5	23.3	1013	4	US-09-612-402B-16	Sequence 16, Appl
21	1098.5	23.0	1013	4	US-09-198-452A-35	Sequence 35, Appl
22	1015.5	21.3	450	4	US-09-198-452A-35	Sequence 35, Appl
23	888	18.6	530	4	US-09-198-452A-482	Sequence 482, App
24	865	18.1	880	4	US-09-556-877-175	Sequence 175, App
25	865	18.1	880	4	US-09-620-412C-175	Sequence 175, App
26	865	18.1	880	4	US-09-598-419-175	Sequence 175, App
27	856	17.9	866	4	US-09-556-877-189	Sequence 189, App

ALIGNMENTS

RESULT 1
US-09-198-452A-29
; Sequence 29, Application US/09198452A

```

: APPLICANT: Griffois, R.
:
: TITLE OF INVENTION: Chlamydia pneumoniae genome
:
: TITLE OF INVENTION: thereof and uses thereof,
:
: TITLE OF INVENTION: and treatment of infection
:
: FILE REFERENCE: 9710-003-999
:
: CURRENT APPLICATION NUMBER: US/09/198.452A
:
: CURRENT FILING DATE: 1998-11-24
:

```

Query Match 58.7%; Score 2802.5; DB 4; Length 597;
Best Local Similarity 93.8%; Pred. No. 2.4e-204;
Matches 560; Conservative 5; Mismatches 21; Indels 11.

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QY 569 FHVYQGTWGPVWGTGASTTATFNWTKTGYIPNPERIGSLVPSNLNNAFIDISSLHYLM 628
Db 421 FHVYQGTWGPVWGTGASTTATFNWTKTGYIPNPERIGSLVPSNLNNAFIDISSLHYLM 480
QY 629 ETANEGLOGDRAFWAGCAGLSNFFHDKSTKTRGRFHLSGVYVIGGNLHTCSDKILSAAPCQ 688
Db 481 ETANEGLOGDRAFWAGCAGLSNFFHDKSTKTRGRFHLSGVYVIGGNLHTCSDKILSAAPCQ 540
QY 689 LFGDRDRDYFAVAKNQ--TVGGTGLYYQHNETYIS-----LPCCLR-PCSLSYVP 734
Db 541 LFGDRDRDYFAVAKNQRLSRLRRSLPAQRNLYLSLQTTALFVVLGSCYSDRSCSLFRKP 597

RESULT 2
US-09-198-452A-470
; Sequence 470, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-470

Query Match 40.6%; Score 1940; DB 4; Length 930;
Best Local Similarity 43.7%; Pred. No. 1.4e-138;
Matches 416; Conservative 165; Mismatches 324; Indels 48; Gaps 17;
QY 1 MKSSPPKFFVSTFAIPPLSM--IAT--ETVLDSSAFDGNKNGNFGSVRESQEDAGTYILF 56
Db 1 MKIPLKLLISLTVPIILLISATYADASLSPTDFDAGGSGTTPPKSTADANGTYNVL 60
QY 57 KGNVLTENIPGTGTAITKSCFNNTKGLDFTNGNSLLFQTVDAVAGAAVNSVVDKS 116
Db 61 SGNVYI-NDAGKALTGCGFTTGTDLTFTGKGYFSFNTVDAGSNAGAAA-STTADKA 118
QY 117 TPIGFSLSFIASPOSSITTKGAVSCSTGSLTKVNSLLESKNEFTD---NGGALTA 173
Db 119 LTFTGFSNLSFIAAPGTTVASGKSTLS-SAGALNLTNGTILFSQVNSNEANNNGALTA 177
QY 174 KTLSLCTWMSALFSENTSKKGAICOTSALITITNGQGVFSFSDNTSSDSGAAIFTEAS 233
Db 178 KTLISGNTSSITFTNSAKLGGAIYSSAAISIGNTGQVFPNNKGETGGGALGFEAS 237
QY 234 VTISNNAKVFDINKVTGASSTTGMDSGGAICAYKTSSTDKVTLTQNMQLLSNNVTSTT 293
Db 238 SSITQNSLFFSGNTATDAAG-----KGGAIYCEKGETPTLTISGNKSLITFAENS SVT 291
QY 294 AGGAIYVKKLELAGGGLTLFSRNVNGTAPKGAIAIEDSGELSLSDSGDIVELGNTV 353
Db 292 QGGAICAHLGLDLSAAGTTLFSNNRCGNTAAKGAIAIADSGSLSLSANQGDITFLGNTL 351
QY 354 TSSTT-PTGNRSSIDLGTSAKWTALRSAGRAIYFDPI---TTGSSTTTVDLVKVNTPA 409
Db 352 TSSTAPTSTRNAILYGGSAKITNLRAGQGSIIYFDPIASNTTCAS---DVLTIQNPDS 407
QY 410 DSALQYTGNIITFTGKLESEPAADSKNLTSKLQPVTLGSGGTLISLKGVTLOQAFTQQA 469
Db 408 NSPLDYSCTIVFSGEKLSDAEKAAADNPTSILKQPLASGTLALKGNVELDVNGFTQTE 467
QY 470 DSRLEMDVGTILEPADTSTIN--NLVINISSIDGAKKAKIETKATSKNLTSLGTTILDP 527
Db 468 GSTLLMQPGTKLK-ADTEAISLTKLIVDLSSALEGNKSVSIETAGANKITILTSPLVFQDS 526
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QY 528 TGTFFYENHSLRNPOSYDILELKAS-----GTVTSTAVTPDPIMGEKPHYGYQGTWG 578
Db 527 SGNFYESHTTINQAFQTQPLVWFTATAAASDIYDALLTSVPQTPEP-----HYGVQGHWE 580
QY 579 PIWGTGASTTATFNWTKTGYIPNPERIGSLVPSNLNNAFIDISSLHYLMETANEGLQD 638
Db 581 ATWADTSTAKSGTWTWTTGYNPNPERRASVVPDSLWASFTDITRLOQIMTSQANSIYQQ 640
QY 639 RAFWAGCAGLSNFFHDKSTKTRGRFHLSGVYVIGGNLHTCSDKILSAACOLFGDRDRDYFV 698
Db 641 RGLWASGTANFFHDKSGTQNAFRHKSYGYIVGSAEDFSENI FSAVAFQFGKDKDLFI 700
QY 699 AKNQVTVGGTGLYYQHNETYISLPCCLR-PC--SLSYVTEIPVLPSGNSLYTHTDNDLKT 756
Db 701 VENTSHNYSLSLYLQHRAFLGGLP---MPSPGSIIDMLKDIPLIILNAQLSYTYKNDMDT 757
QY 757 KYTTVPTVKSGWGNDSFALEFGGRAPICL-DESALFEQYMPFMKLOFYVAHQEGKPEQGT 815
Db 758 RYTSYPEAQQSWNNNSGALGLGSLALYLKPEAPFFQGYFFELKFAVYVSRQNFESGA 817
QY 816 EAREFGSRLVNLAIPIGIRPDKESDCQDAYNLTGYTVDLVRSNPDCITTLRISGDSW 875
Db 818 EARAFFDDGDLVNCSPVIGIRLEKISEDEKNNFELSLAYIGDVYRKNPRTSLMVGASW 877
QY 876 KTFGCTNLARQALVLRAGNHFCFNSFEAFSOPFELGSSRRNRYNDLCAKYOF 928
Db 878 TSLCKNLARQAFIASAGSHLTLSPHVELSGEAAHYELRGSALHYNVDCGLRYSF 930

RESULT 3
US-09-198-452A-472
; Sequence 472, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 472
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; NAME/KEY: SITE
; LOCATION: 1...927
; OTHER INFORMATION: Xaa-unknown or other
US-09-198-452A-472

Query Match 40.2%; Score 1917.5; DB 4; Length 927;
Best Local Similarity 44.8%; Pred. No. 7.2e-137;
Matches 427; Conservative 147; Mismatches 328; Indels 51; Gaps 22;
QY 1 MKSSPPKFFVSTFAIPPLSM-----IATETVLDSSAFDGNKNGNFGSVRESQEDA-GTT 53
Db 1 MKSSLHFLISSLSLALPLSLNLSFAFAAVVEINLGPNTSPSG--PGTYTPPAQTNAQGTI 58
QY 54 YLFGKGVNLTENIPGTGTAITKSCFNNTKGLDFTNGNSLLFQTVDAVAGAAVNSSVV 113
Db 59 YNLTGDDVSIYN-AGSPALTATSCPETKTNLSFGHGYQFLLQNDAG--ANCTFTNTAA 115
QY 114 DKSTFTTIGFSSLSFIASPGSSITTKGAVSCSTGSLTKVNSLFLSKNLTSTONGALTA 173
Db 116 NKLLSFGSFSYLSLIQT--TNAITGTGAIK-STGACSIQSNYSYCYFGCNFNDNGGALQG 172
QY 174 KTLSLTGTWMSALFSENTSKKGAICOTSALITITNGQGVFSFSDNTSSDSGAAIFTEAS 233
Db 173 SSISLS-LNPNLTFAKNKATQKGALYSTGGITINTNLNSASFSENTAANNNGALYTEAS 231
QY 234 VTISNNAKVFDINKVTGASSTTGMDSGGAICAYKTSSTDKVTLTQNMQLLSNNVTSTT 292
```

Db 232 SFISSNKAISFINNSVTATSA-----TCGAIYCSSTSAKPVLTLSDNGELNFGNTAI 285
 Qy TAGGAIYVKLELASSGLTLFSRNSVNGTAPKGAIAIEDSGELSLSDADSDIVFLGNT 352
 Db 286 TSGGAIYDNLVLSGGTFLFNNSAIDTAAPLGAIAIADSGLSLSALGDDITFEGNT 345
 Qy 353 V---TSITPGNRSIDIG-TSAKMTALRSAGRAIYFYDPIITGSSSTTVTDVLKVNTP 408
 Db 346 VVGASSQTTRNSINIGNTNAKIVQLRASQCNITFYDPIITTSITAALSDALNINLGP 405
 Qy 409 ADSALQYTGNIIFTEGKLESETEADSKNLTSLKLPVTLSSGTLKHGVTILQTAFTQQ 468
 Db 406 LAGNPAVQGTIVFGEKLESEAEADNLKSTIOOPLTAGGQLSLKSGVTLVAKSFQS 465
 Qy 469 ADSLEMDVGTTLBPADTSTINNLVINISSIDGAKAKIET-KAT--SKNLTLSGTLILL 525
 Db 466 PGSTLLMDAGTTLTADGS-----LSIICSQCFLKRDQEXLTKATASQTVILSGSLV 521
 Qy 526 DPTGTFYENSLRNPQSYDILELKAS--GTVTSFVAVTPDPIMGBKFGHYGQGTWGPVWG 583
 Db 522 DPGSNVYEDVSWNNPQVFSCLTITADDPANIHTDLAADPLEKNPIHWGYQGNWA-LSWQ 580
 Qy 584 TGAST---TATENWTKGYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLOQDRA 640
 Db 581 EDATKSKAAHLTWKTYGPNPERRGTLVANTLWGSFVDVRSIQQLVATKVRQSQETRG 640
 Qy 641 FWCAGLSNFFHKDSTKTRRGRHLSSGGYVIGGNLHTCSDKILSAACQLFRDRDYFAK 700
 Db 641 IWCEGINFFHKDSTKINKGRHISAGYVVGATTLASDNLITNAFQLFGKDRHFINK 700
 Qy 701 NOGTVYGGTLYYQHNETYIISLPCKLRPCSLSYVP---TEIPVLFSGNLSYTHDNDLTK 757
 Db 701 NRASAYAAASHLOHLATLSS-----PSLLRYLPGSESEQVPLFDAQIYIYSKNTMKY 754
 Qy 758 YTYPTVKGSGWNSPALFEGGRAP-ICLDSEALFEQYMPFMKLOFYVAHQEGFKQGT 816
 Db 755 YTOAPKGESSWYNGGCALEASLPHLALSHGELFHAYFFFIKVEASYIHQDSFKERN 814
 Qy 817 -AREFGSSRLVNLALPIGIRFDKESQCDATYNTLGYTVDLVRSNPDCTTLRISGDSW 875
 Db 815 LVRSFSDGLINVSPIGITFEFRSNERASYATVIYVADVTRKPDCTTALLINNTSW 874
 Qy 876 KTFGTLARQALVLRAGNHFCEFNSEAFQSFELRGSSRNYNVDIGAKYQF 928
 Db 875 KITGTNLSRQAGTGRAGIFAYFSPNLEVTSLNLSMEIRGSSRSYNADLGGKQF 927

RESULT 4

US-09-198-452A-478
 ; Sequence 478, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 478
 ; LENGTH: 949
 ; TYPE: PRN
 ; ORGANISM: Chlamydia pneumoniae
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: 1...949
 ; OTHER INFORMATION: Xaa=unknown or other
 US-09-198-452A-478
 Query Match 38.9%; Score 1856; DB 4; Length 949;
 Best Local Similarity 42.7%; Pred. No. 3.5e-132;

Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;
 Qy 1 MKSFPKVFVFSTFAIPP--LSMIATETVLDSASAFDGN-KGNFNSVRESQEDAGTYYLTK 57
 Db 22 MKTSIPMWLVSVLAFSCHLQSLANEHLLSPDDFNGNIDSGTTPKTS---ATTYSILT 77
 Qy 58 GNVTLLENIPGTGATLTKSCFNNTKGLDTFTGNGSLLPQTVDAGTVAGAAVNSVVDKST 117
 Db 78 GDVFFYE-PGKGTPLSDSCFQKQTTDNLTLFLNGHSLTFEGFDAGTHAGAAA-STTANKNL 135
 Qy 118 TFIQFSSLFSTIASPGSSITTCGKAVSCSTGSLSTKTNVLSLFSKNFSTDNGCAITAKLS 177
 Db 136 TFGSFLSLSPDSSPTVTITGQGTLS-SAGGVNLENIRKLVVAGNFSTADGAIGKAGSFL 194
 Qy 178 LTGTTMALPSENTSSKKGAIQTSDALITITGNGEVSFSDNTSSDGAALIFTEASVTIS 237
 Db 195 LTGTSGDALFSNNSSTKGAIAATTAGAIANNNTGXVFLSNIASTSGAIDDEGTSILS 254
 Qy 238 NNAKVSFIDNKVTGASSSTTGDMSSGGAICAYKTSITDTKVTITGNQMLLFSNNTSTAGGA 297
 Db 255 NKKELYP-----EGNAAKTT----GGAIKNTKASGSPELIISNNKTLIFASNVAETSGGA 305
 Qy 298 IYVKLELASGGLTLFSRNSVNGTAPKGAIAIEDSGELSLSDADSDIVFLGNTVST- 356
 Db 306 IHAKKALSSGGTTEFLRNNVSSAT-PKGAISIDASGELSLSABTGNITFVRNLTITG 364
 Qy 357 -TGTNRSSIDLGTSAKMTALRSAGRAIYFYDPIITGSSSTTVTDVLKVNETPADSALOY 415
 Db 365 STDTPKENAINISNGKFTELRAAKNHTIFFYDPIIT--SEGTSSDVLKINNGSAGALNPY 422
 Qy 416 TGMNIIFTGEKLSATEAADSKNLTSLKLPVTLSSGTLKHGVTILQTAQADSLKEM 475
 Db 423 QGTILFSGEGLTDADELKVAIDLKSSFTQPVLSGGKILLQKGVTLSESTFSQAGSLILGM 482
 Qy 476 DVGTILLE-PADTSTINNLVINISSIDGAKAKIETKATSKNLTLSGTLITLDPGTGYEN 534
 Db 483 DSGTTLSTTAGSITIINLGINVDSLGLKQVPSLTAKGASKVIVSGKLNLDIEGNIYES 542
 Qy 535 HSURNPQSYDILELKASGTVTS---TAVTPDPIMGEKFGHYGQGTWGPVWGTVGASTT- 589
 Db 543 HMFSDHQLFLSLKITVDADVDTNVDISSLIPVPAEDPNSEYGFQGMW-VNWTDTATNT 601
 Qy 590 --ATFNWTKGYIPNPERIGSLVPSNLWNAFIDISSLHYLMETANEGLOQDRAFWCAGLS 647
 Db 602 KEATATWTKGVFPSPERKSALVCNLTWGVFTDIRLQQLVETGATCMKHEKQGFVSSMT 661
 Qy 648 NPFHKDSTKTRRGRHLSSGGYVIGGNLHTCSDKILSAACQLFRDRDYFAKNOGTVYG 707
 Db 662 NFLHKTGDENRKGFRHTSGGYVIGGSAHTPKDLDLTFEAFCHLFARXKDCFAIHNNTYTG 721
 Qy 708 GTLYYQHNET-----YISL-PCKLRPCSLSYVTEIPVLFSGNLSYTHDNDLTKYTTY 761
 Db 722 GTLFFKHSHTLQPNYLRIGRAKFSSEAEKPREIPLADLVQVFSFSDNRNMEHTYSL 781
 Qy 762 PTVKSGWNSPALFEGGRAPICL-DESALFEQYMPFMKLOFYVAHQEGFKQGTAREP 820
 Db 782 PESEGSWSNECIAGGIGLGLDLPVLSNPHLPFKFTIPQMKVEMVYVSQNSFFSSSDGRG 841
 Qy 821 GSSRLVNLALPIGIRFDKESQCDQA-TYNLTLYTVDLVRSNPDCTTLRISGDSWKTFG 879
 Db 842 SIGRLNLSIPVGAKEF-VQGDIGDSYTYDLSGFFVSDVYRNNPQSTALVWGPDSWKING 900
 Qy 880 TNLARQALVLRAGNHFCEFNSEAFQSFELRGSSRNYNVDIGAKYQF 928
 Db 901 GNLSRQAFLLRGSSNNVYNSNCELFGHVAMELRGSSRNYNVDVGTKLRF 949

RESULT 5

US-09-198-452A-474
 ; Sequence 474, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffiths, R.

Tue Aug 17 09:45:49 2004

us-09-428-122-2.ra1

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; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 474
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-474

Query Match      32.9%; Score 1572.5; DB 4; Length 643;
Best Local Similarity 49.8%; Pred. No. 6.3e-111; Indels 15; Gaps 6;
Matches 314; Conservative 93; Mismatches 209;

Qy 308 GGLTLFSSNVNGGTAPKGAIAIEDSGELSLSDSGDIVFIGNVTSTTP-GTNRSSID 366
Db 18 GGGISFNNIVQGITAGNGGALSILAAGECSLSAEAGDITENGNAIVATTPTQTKRNSID 77
Qy 367 LGTSKMTALSAAGRAIYFYDDPIITGSSSTTVTVLKVNETPADSALQYTGNIIFTGKEL 426
Db 78 IGTAKITNLRAISGHSIFFYDPIITANTAADSTDTLNLNKADAGNSTDYSGSIVSFGKEL 137
Qy 427 SETEAADSKNLTSKLLQPVTLSSGGLSLKHGVTLOTQAFQOADSRLMDVGTITLEPA-D 485
Db 138 SEDEAKVADNLVSTLQKPVTLTAGNLVLRGVTLDTGFTQTAGSSVINDAGTTLKASTE 197
Qy 486 TSTINMLVINISSIDGAKAKIETKATSKNLTLSTGTTITLDDPTGTFYENHSLRNPQSDYI 545
Db 198 EYTLTGLSLTPVDSLGEKKVVAASAASKNVALSGPILLDDQGNAYENHDLGKTQDFSF 257
Qy 546 LELKASGVTVSTAVTPDDPMGKFKHYGYQGTWGW-----GTGASTTATTNNKTYGI 600
Db 258 VQLSALGTATTDDVPAVPTVATPTHYGYQGTWGW-MTWVDDTASTPKTKATLAWNTIGYL 316
Qy 601 NPERIGSLVPSNLNNAFTDSSHLVLMETANEGLQDRAFCAGLSNFFHDKSTKTRRG 660
Db 317 PNPEKQGPLVPSNLGSGFSDIOAQIVERSALTCDSDRGFWAAGVANFLDKDKKGEKK 376
Qy 661 FRLHSGYVIGGNLHSCDKILSAFQCFGRDRDYFVAKNQGTGVGGLTYVQHNETYS 720
Db 377 YRHKSGYAIAGGAQTCSENLSIFAFQCFGSKDPLVAKNHTDTYAGAFYIQH-----IT 432
Qy 721 LPOKLRPCSLVYP-----TEIPVLFSGNLSYTHDNDLTKYTYTYPTVKGSGWSDSFALEF 777
Db 433 ECSGFTGCLLDKLPGSWSHKPLVLEGQLAYSHVSNLDLTKYATPEYKSGSWGNNAFMML 492
Qy 778 GGRAPICLDESALFEOYMPMKLOFVYAHQEGFKQGTAREFGSSRLVNLALPIGIRFD 837
Db 493 GASHSYPEYLHCFDYAPYIKNLTYIRQDSSEKGTGERSFDDSNLNLPIGVKFE 552
Qy 838 KESDCODATYNLGTLYTVLVRNPDCTTLRISGDSWKTFTGNLRAQALVLRAGNHCFP 897
Db 553 KFSDCNDFSVDLLTSYVDDLIRNDPKCTTALVSGASWETAYANLARQALQVRAGSHYAF 612
Qy 898 NSNPEAFSPQSFEIRGSSRYNVDLGAKYQF 928
Db 613 SPMFEVLQGFVEVRGSSRYNVDLGKQFQF 643

RESULT 6
US-09-198-452A-15
; Sequence 15, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A

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; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 15
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...922
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-15

Query Match      29.7%; Score 1417.5; DB 4; Length 922;
Best Local Similarity 36.5%; Pred. No. 6.4e-99;
Matches 347; Conservative 156; Mismatches 385; Indels 63; Gaps 26;

Qy 5 FPFKVFSTFAIFPLSMIATETVLDDSSASFQGNKNGFVSRESQEDAGTTLFKGNVTLE 63
Db 8 FPLVFSFTLLSVFDTLSATLITLTPEDSPHGDQN--AERSYNVQAGDVYSLTGDVSI 65
Qy 64 NIPGTGTAITKSCFNNTKGDITFTGNSLLPQTVDAGTVAGAAVNSVVDKSTT-FIGF 122
Db 66 NV--DNSALNKACPKVTSVTFAGNHGXFYFNISGTTKEGAVLCCODPOATARFSGF 123
Qy 123 SLSFIASPGSITTKGAVSC--STGSLSLTKNWSLLFSKNFSTDNGGAIKATLSLTG 180
Db 124 STLSPGPGDIKEQG-----CLYSKNALMLNNVVVFEQNKTKGGAISGANVTIVG 178
Qy 181 TTMSALFSENTSSKKGAIQTSDALTITGNOGEVSFSDNTSSD-SCAAIFTASVTISNN 239
Db 179 NYDSVSFYQNAAT-FGGAIHSSGPLQIAVNOAEIRFAQNTAKNGSGGALYSDGIDIDQN 237
Qy 240 AKVSFIDNKVTGASSSTTGDMSGGAI CAYKSTDTK----VTLTGNQMLLFSNNTSTTAG 295
Db 238 AVVLFRENE-----ALTTAIGKGA VCCLTPTSGSSTPVPVTFPSDNKQLVFRNHIMGG 292
Qy 296 GAIYVKLELASGGLTLFSRNSVNGTAPKGAIAIEDSGELSLSDSGDIVFLGNTVTS 355
Db 293 GAIYARKUSISSGGPTLFNNISYANSQNLGGAIALDTGGEISLAEKGTIIFQGN--RT 350
Qy 356 TTPGTNRSSIDLGTSKMTALSAAGRAIYFYDDPIITGSSSTTVTVLKVNETPADSALQY 415
Db 351 SUPFLN--GIHLQNAKFLKLOARNGYSIEFYDPIIT--SEADGSTQLNIDGPKNK--EY 404
Qy 416 TGNITPTGKLSETEAADSKNLTSKLLQPVTLSSGGLSLKHGVTLOTQAFQOADSRLM 475
Db 405 TGTILPSGEK--SLANDPRDFKSTIPQNVNLSAGYLVIKEGAETVTSKFTQPGSHLV 461
Qy 476 DVGTTIL-EPADTSTINNLVINISSIDGAKKAK-IETKATSKNLTLSTGTTITLDDPTGTFYE 533
Db 462 DLGTKLIASKEDIAITGLAIDIDLSLSSSSTAIVIKANTANKQISVTDSELIISPTGNAYE 521
Qy 534 NLSLRNPQSDYIILELK--ASGTVTSTA-----VTPDPIMGKFKHYGYQGTWGPVIV-GTG 585
Db 522 DLMRRNSQIFPLLSLEPGAGSVTVTAGDFLPVSP-----HYGFQGNW-KLAWTGTG 572
Qy 586 ASTATFNNWTKTYIENPERIGSLVPSNLNNAFTDSSHLVLMETANEGLQDRAFCAG 645
Db 573 -NKVGEFFWDKINYPKPEKEGNLVPNLMGNNAVDVRSIMQVQETHASSLQTDRLGLWDG 631
Qy 646 LSNPFHKDSTKTRRGRHLSGGYVIGGNLHSCDKILSAFQCFGRDRDYFVAKNQGTV 705
Db 632 IGNLFHVSASEDNIRYHNHSGGVLSVNNETPKHYTSMAFSOLFSDKDYAVSNNEYRM 691
Qy 706 YGGTLYYQHNET-----YISLPCKLRPCSLSVYPTPIP-VLPSGNLSYTHDNDLTKY 758
Db 692 YLGSYLYQYTTSLGNITPRYASRNPVNVGILSRFLQNLPLMIFHLFCAYGHATNDMTDY 751
Qy 759 TTPVTYKSGWNSFALFEGGRAPICLDESA-LPEQYMPMKLOFVYAHQEGFKQGTGTEA 817
Db 752 ANFPWKNVSRNRCNWAIECGSGMPLLVFENGRLFGGAIPFMKQLQVYAYQGFKEETADG 811
Qy 818 REFSSRLVNLALPIGIRFQKESDCODATYNLGTLYTVLVRNPDCTTLRISGDSWKT 877

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Qy	295	GGAIYVKLELASGGLTLFSRNSVNGTAPK--GGAIAIEDSGELSLSDAGDGVFLFGLNT	352
Dd	293	GGAISGLUKVLSASGPPILFQSN-LSGSAGCGGGAINIASAGELALSATSODITFNQK	351
Qy	353	VTSPTPGNRRSSIDLGTSAKMALRSAAGRAIYFYDPITTTGSGSTTVTVLKNETPADSA	412
Dd	352	VTNGSST-RNAINIIDTAKVTSIRAATQSQSYFYDPITTPGTAASTDTLLNLADANSE	410
Qy	413	LQYTGNLIIFTEKLSSETAADSKNLTSLKLQPVLTLSGGTSLKHGHVTLQTQAFTOQAUSR	472
Dd	411	I EYGAIIVFSGEKUSPTEKALAANVISIRQPAVLARGDLVLRDGVYVTFKDILTQSPGR	470
Qy	473	LEMVGTTILEPADTS-TNNLVINISSIDGAKKAKIETKATSKNULTSGTITLLDPTGTF	531
Dd	471	ILMDGGTILLSAKEANLSINGLAUVNLSSLDGNTKAALKTEAADKNISLSTGIALIIDTEGSF	530
Qy	532	YENHSLRNPSQYDIIELEK---ASGVTSTAVTPDDPMGEKPHYQGVTWGPVWGTCGST	588
Dd	531	YENHLNKASTYPLLELTITAGANGTIITLGALSTFLIQEPETHYGYQGNW-QLSWANATSS	589
Qy	589	-TATFNWTKTGYIPNPERIGSLVPNSLMNAFIDISLHYLMETANEGLOGCDRAF	641
Nt	590	KIGSNWRTGTGYIPERKSNIPLNSMGWNFIIDRSINOLIIETKSSGEFFEREY	643

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RESULT 9
US-09-198-452A-30
; Sequence 30, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffoais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION:
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 30
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-30

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	Query Match	25.4%;	Score 1214;	DB 4;	Length 230;	
	Best Local Similarity	99.6%;	Mismat.No. 2.1e-84;			
	Matches 226;	Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	702	QGTVVGGTLYYOHNETYISLPCKLRPCSLSYVPTPEIPVLFSGNLSYTHTDNDLTKKTYTT	761			
Dd	:	:::::				
Qy	762	PTVKSGWGNDSFALPFGGRAPICLDSEALFEQYMFMKLQFYVAHQEGFKCGTEAREFG	821			
Dd	64	PTVKSGWGNDSFALPFGGRAPICLDSEALFEQYMFMKLQFYVAHQEGFKCGTEAREFG	123			
Qy	822	SRLVNLAIPGIRDEKSDCCDQATNYLTGLTVDLVRSPNPDCTTTLLISGDGSKWTFCGN	881			
Dd	124	SRLVNLAIPGIRDEKSDCCDQATNYLTGLTVDLVRSPNPDCTTTLLISGDGSKWTFCGN	183			
Qy	882	LARQALVLRAGNHCFNSNFEAFFSFPFLRGSSRNNVNDLGAKYQF	928			
Dd	184	LARQALVLRAGNHCFNSNFEAFFSFPFLRGSSRNNVNDLGAKYQF	230			

RESULT 10

US-09-198-452A-32

; Sequence 32, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; STATE OF INVENTION: Chlamydia pneumoniae

```

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis
; FILE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 32
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-32

```

Query Match	25.2%	Score 1203.5	DB 4	Length 507
Best Local Similarity	46.9%	Pred. No. 4.5e-83		
Matches	235	Conservative	82	Mismatches 165
				Indels 19
				Gaps 7
Qy	436	NLTSLKLPVTLSSGTTLSLKHGVTQLQAFQQAADSRLEMDVGTTLE-PADTSTINNLLVI	494	
Db	18	NLKSFTTQAVELAGALVLKGVTVVANTITQVEGSKVMDGGTTTPEASAEGVTLGLAI	77	
Qy	495	NISSIDGAKKAKIEFKATSKNLTLSGTTITLDPDPTGYENHSLRNPOSYDILELKASGTV	554	
Db	78	NIDSLDGNTKAI IKATAASKDVALSGPIMLVDAQCNVYEHNLSSQQVFFALIELSAQGM	137	
Qy	555	TSTAVTDDPIMGEFHHGYQGTWGPVW--GTGASITATFNWTKTGYIPNPERIGSLVP	611	
Db	138	TTTIDPPTPIINTNNHGIKGT-GIIIVWDDATKNTKATLTWTKTGYKNPERQGVLVP	196	
Qy	612	NSLWNAFIDISLHVLMTANEGLQGDRAFCAGLSNPFHFKDSTKTRRGFHLSSGGYVIG	671	
Db	197	NSLWGSFVDDVRSIOSLMDRSTSSLSSTNLWVSGIADFLHEDQKGNQRSYRHSSAGYALG	256	
Qy	672	GNLJHTCSKILLSAFCQLFGDRDRDYFVAKNOGTVVGGTLYYQH---NETYISLPCKLRPC	728	
Db	257	GGFTASENFNFNAFCQLFGYDKHLVAKNHTHVYAGAMSYRHLGESKTLAKI-----	309	
Qy	729	SLSYVPTPI PVLFGSNLSYTHDNDLTKYTTPTLVKSGWGNDSFALRGGRAPICLD-E	787	
Db	310	-LSGNSDSLPPFVFNARFAYGHTDNNMTTKTYGSPVKSGWGNDAFGICGGRAIPVVASGR	368	
Qy	798	SALPEQYPMFKLPQVYAHOGFKEQGEAREFGSSRLNLTALPTGIRFDKESDQCDATY	847	
Db	369	RSWVDTHTPFNLNLEMIYAHQNDFKENGTEGCRSFQSEDLFNLAVPVGINKFEKFS	426	
Qy	848	NLTGLTYVDLVRNSPDCITTLIRISGDSWKTFGTNLARQALVLRACNHPCFNNSFAFSQF	907	
Db	427	DLISIAVDPVDIENDPGCTITLWVSGDSNSTCGTSLRQALLVRAGNHAFASNFVFSQF	486	
Qy	908	SPELRGSGRNVDLGAKYQF	928	
Db	487	EVELRGSSRSYALDGGRRGF	507	

RESULT 11
US-09-198-452A-466
; Sequence 466, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae
; TITLE OF INVENTION: thereof and uses
; TITLE OF INVENTION: and treatment of
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 466
; LENGTH: 1132
; TYPE: prt
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-466

Query Match 23.7%; Score 1130; DB 4; Length 1132;

Tue Aug 17 09:45:49 2004

QY	591	TF----	NWTKGTIPNPERIGSLVPSLWNAFIDISSLHYLMETANEGLQGDRAFWCAGL	646
Db	679	PYTLKATWTKTGYNPGPEVVASLVPSLWGSILDIRSAHSAIQASVDCRSYCRGLWVSGV	738	
QY	647	SNFPHKSTKTRRGRPHLGGYVIGGNLHTCSDKILSAAFCQLFGDRDRDYFAKNQGTYY	706	
Db	739	SNFFVHDRDALGQGYRYISGGYSLGANSYFGS-SMFGLAFTFVFGRSKDYVVCRSNHHAC	797	
QY	707	GGTLYYQHNETYISLPCKLRPCSLSVVPTFIPVLFSG--NLSYTHDNDLTKYTTYPT	763	
Db	798	IGSVYLSLSTQQAL-----CG-SY-----LFGDAFIRASYGFGNQHMKTSYTFAE	840	
QY	764	VKGSWGNDSFALEFGGRAPICIDEHALF-EQYMPFMKLQVYVAHQEGFKEQGTAREFGS	822	
Db	841	SDVRWNNCLAGEIGAGLPVITPCKLYINELRPVQAEFSYADHESFTEEGDQARAPKS	900	
QY	823	SELVNLALPIGIRFDKESDQDATYNLTLGYTVDLVRSNPDCTTTLRISGDSWKTFTGNL	882	
Db	901	GHLNLNLSVPVGKFDRCSTHFNKYSFMAAYICDAYRTISGTTTLLSHQETWTTDAFHL	960	
QY	883	ARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNYNVDLGAKYQF	928	
Db	961	ARRGVVVRGSMYASLTSNIEVYGHGRYRYRDASRGYCLSAGSKVRF	1006	

Search completed: August 10, 2004, 13:15:24
Job time : 26 secs